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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 10, 2003, 06:16:29 ; Search time 3098 Seconds
(without alignments)
10765.596 Million cell updates/sec

Title: US-09-901-910-1
Perfect score: 1146
Sequence: 1 atgagctcccgcatcgccag.....ttcacaaatttagggactaa 1146

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1146	100.0	1146	6	E13814	E13814 cDNA encodi
2	1146	100.0	1935	9	AF003594	AF003594 Homo sapi
3	1146	100.0	1985	9	BC001271	BC001271 Homo sapi
4	1146	100.0	2016	6	AX336386	AX336386 Sequence
5	1146	100.0	2016	6	AX354335	AX354335 Sequence
6	1146	100.0	2016	9	HSU62015	U62015 Homo sapien
7	1146	100.0	2021	9	HSGIG1PRT	Y12084 H.sapiens m
8	1146	100.0	2025	9	HSCYR61M	Z98053 Homo sapien
9	1146	100.0	2041	9	BC016952	BC016952 Homo sapi
10	1146	100.0	2046	9	BC009199	BC009199 Homo sapi
11	1144.4	99.9	2052	9	HSCYR61	Y11307 H.sapiens C
12	1142.8	99.7	1418	6	AX206704	AX206704 Sequence
13	1142.8	99.7	2270	6	AX035239	AX035239 Sequence
14	1142.8	99.7	2270	6	AX342093	AX342093 Sequence
15	1142.8	99.7	2270	6	AX342153	AX342153 Sequence
16	1142.8	99.7	2270	6	AX441156	AX441156 Sequence
17	1141.2	99.6	1887	9	AF031385	AF031385 Homo sapi
18	1075.6	93.9	1128	6	AX463811	AX463811 Sequence
19	907.2	79.2	1220	9	AF003114	AF003114 Homo sapi
20	896	78.2	1480	6	AX206702	AX206702 Sequence
21	896	78.2	2018	10	MUSCYR61A	M32490 Mouse Cyr61
22	894.4	78.0	1987	10	AF218568	AF218568 Rattus no
23	888	77.5	1871	10	AB015877	AB015877 Rattus no
24	663.4	57.9	1805	5	CHKCEF	J04496 Chicken CEF
25	615.6	53.7	1860	9	AK096420	AK096420 Homo sapi
26	615.6	53.7	180574	9	AC092807	AC092807 Homo sapi
27	606.4	52.9	4468	9	AF307860	AF307860 Homo sapi
28	567.4	49.5	1743	5	AF320592	AF320592 Xenopus l
29	513	44.8	806	6	AX210560	AX210560 Sequence
30	505	44.1	1687	9	HSM804202	AL832891 Homo sapi
31	325.6	28.4	173461	2	AC126890	AC126890 Rattus no
32	302.4	26.4	304	9	HSA33210	Z50168 H.sapiens p
33	288.6	25.2	5196	10	MMCYR61G	X56790 Mouse growt
34	214	18.7	255	6	AX210743	AX210743 Sequence
35	205.8	18.0	2190	5	AF463517	AF463517 Gallus ga
36	205.8	18.0	2288	5	GGA298335	AJ298335 Gallus ga
37	204.4	17.8	2075	6	AR018957	AR018957 Sequence
38	204.4	17.8	2075	6	AR118595	AR118595 Sequence
39	204.4	17.8	2075	6	AR130891	AR130891 Sequence
40	204.4	17.8	2075	6	AX206708	AX206708 Sequence
41	204.4	17.8	2075	6	I11636	I11636 Sequence 1
42	204.4	17.8	2075	6	I32210	I32210 Sequence 1
43	204.4	17.8	2075	9	HUMCONGRO	M92934 Homo sapien
44	204.4	17.8	2312	9	HSCTGF	X78947 H.sapiens m
45	204.4	17.8	2998	6	AR119211	AR119211 Sequence

ALIGNMENTS

RESULT 1
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LOCUS E13814 1146 bp DNA linear PAT 27-APR-1998
DEFINITION cDNA encoding human macrophage-maturing and differentiating factor (MMDF).
ACCESSION E13814
VERSION E13814.1 GI:3252582
KEYWORDS JP 1997234079-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1146)
AUTHORS Ooi,K., Satsu,T., Kizumoto,M., Hara,H., Seki,T., Shimonishi,M., Nagasawa,T., Sakai,H., Shimizu,N. and Hagiya,M.

```
  TITLE     MONOCYTIC MATURATION DIFFERENTIATION FACTOR
  JOURNAL   Patent: JP 1997234079-A 1 09-SEP-1997;
            TOYOBO CO LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 1997234079-A/1
            PD   09-SEP-1997
            PF   04-MAR-1996 JP 1996075236
            PI   OOI KIYOMOTO, SATSU TAKASHI, KIZUMOTO MASAMI, HARA HISANORI,
            PI   SEKI TATSUYA,
            PI   SHIMONISHI MANABU, NAGASAWA TETSUJI, SAKAI HARUMI, PI
            SHIMIZU NORIHIDE,
            PI   HAGIYA MICHIO
            PC   C12N15/09,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,
            PC   C07H21/04,
            PC   C07K14/47,C07K14/52,C12N5/10,C12P21/02,(C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            FH   Key             Location/Qualifiers
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            FT   source          1. .1146
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            FT                   /cell_type='thyroidoma'
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            FT   mat_peptide     1. .1143
            FT                   /product='human macrophage-maturing and  FT
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     source           1. .1146
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 2.6e-235;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
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Db          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60

Qy         61 CTGGCGCTCTCCACCTGCCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
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Db         61 CTGGCGCTCTCCACCTGCCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
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Db        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
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Db        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240

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Db        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840

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Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
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Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
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Db       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140

Qy       1141 GACTAA 1146
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Db       1141 GACTAA 1146


RESULT 2
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LOCUS       AF003594               1935 bp    mRNA    linear   PRI 15-JUN-1997
DEFINITION  Homo sapiens growth-factor inducible immediate early gene product
            CYR61 mRNA, complete cds.
ACCESSION   AF003594
VERSION     AF003594.1  GI:2196781
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1935)
  AUTHORS   Kolesnikova,T.V. and Lau,L.F.
  TITLE     Human growth-factor inducible gene product CYR61, complete sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1935)
  AUTHORS   Kolesnikova,T.V. and Lau,L.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAY-1997) Genetics, University of Illinois, 900 S.
            Ashland Ave., M/C 669, Chicago, IL 60607, USA
FEATURES             Location/Qualifiers
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BASE COUNT      488 a    481 c    510 g    456 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.5e-235;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
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Db        484 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 543

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Db        664 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 723

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
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Db        724 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 783

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
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Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
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Qy       1141 GACTAA 1146
              ||||||
Db       1264 GACTAA 1269
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RESULT 3
BC001271
LOCUS       BC001271                1985 bp    mRNA    linear   PRI 12-JUL-2001
DEFINITION  Homo sapiens, cysteine-rich, angiogenic inducer, 61, clone MGC:5081
            IMAGE:3454581, mRNA, complete cds.
ACCESSION   BC001271
VERSION     BC001271.1  GI:12654854
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1985)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-DEC-2000) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 4 Row: h Column: 9
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4504612.
FEATURES             Location/Qualifiers
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BASE COUNT      503 a    501 c    518 g    463 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 2.5e-235;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
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Db        160 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 219

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
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Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
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Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
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Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
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Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
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Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
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Db        580 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 639

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
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Db        640 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 699

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
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Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
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Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
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Db        820 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 879

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
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Db        880 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 939

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
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Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
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Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
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Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
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Qy       1141 GACTAA 1146
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Db       1300 GACTAA 1305


RESULT 4
AX336386
LOCUS       AX336386                2016 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 6895 from Patent WO0194629.
ACCESSION   AX336386
VERSION     AX336386.1  GI:18127105
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 6895 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .2016
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BASE COUNT      490 a    525 c    534 g    467 t
ORIGIN

  Query Match           100.0%;  Score 1146;  DB 6;  Length 2016;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-235;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
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Db        210 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 269

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
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Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
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Qy       181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
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Qy      1141 GACTAA 1146
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Db      1350 GACTAA 1355
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AX354335
LOCUS       AX354335               2016 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 1 from Patent WO0198359.
ACCESSION   AX354335
VERSION     AX354335.1  GI:18619194
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sampath,D., Zhang,Z. and Winneker,R.
  TITLE     Cyr61 as a target for treatment and diagnosis of breast cancer
  JOURNAL   Patent: WO 0198359-A 1 27-DEC-2001;
            AMERICAN HOME PRODUCTS CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1..2016
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BASE COUNT      490 a    525 c    534 g    467 t
ORIGIN

  Query Match           100.0%;  Score 1146;  DB 6;  Length 2016;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-235;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
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Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
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Db         1290 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1349

Qy         1141 GACTAA 1146
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Db         1350 GACTAA 1355


RESULT 6
HSU62015
LOCUS       HSU62015                2016 bp    mRNA    linear   PRI 28-MAY-1997
DEFINITION  Homo sapiens Cyr61 mRNA, complete cds.
ACCESSION   U62015
VERSION     U62015.1  GI:2130526
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2016)
  AUTHORS   Jay,P., Berge-Lefranc,J.L., Marsollier,C., Mejean,C., Taviaux,S.
            and Berta,P.
  TITLE     The human growth factor-inducible immediate early gene, CYR61, maps
            to chromosome 1p
  JOURNAL   Oncogene 14 (14), 1753-1757 (1997)
   MEDLINE  97280750
   PUBMED   9135077
REFERENCE   2  (bases 1 to 2016)
  AUTHORS   Jay,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-1996) Philippe Jay, Centre de Recherches de
            Biochimie Macromoleculaire, CNRS/INS, Campus CNRS, 1919 route de
            Mende, Montpellier 34033, France
FEATURES             Location/Qualifiers
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BASE COUNT      490 a    525 c    534 g    467 t
ORIGIN

  Query Match             100.0%;  Score 1146;  DB 9;  Length 2016;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-235;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy            1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
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Db          210 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 269

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Db          390 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 449

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Db          510 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 569

Qy          361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
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Db          570 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 629

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Db          630 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 689

Qy          481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
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Db          690 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 749

Qy          541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
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Qy          661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
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Db          990 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 1049

Qy          841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
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Db         1050 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1109

Qy          901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
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Db         1110 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1169

Qy          961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
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Db       1170 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1229

Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
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Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
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Db       1290 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1349

Qy       1141 GACTAA 1146
                ||||||
Db       1350 GACTAA 1355


RESULT 7
HSGIG1PRT
LOCUS       HSGIG1PRT               2021 bp    mRNA    linear   PRI 16-SEP-2000
DEFINITION  H.sapiens mRNA for gig1 protein.
ACCESSION   Y12084
VERSION     Y12084.1  GI:2181870
KEYWORDS    gig1 gene; Gig1 protein.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2021)
  AUTHORS   Albrecht,C., von Der Kammer,H., Mayhaus,M., Klaudiny,J.,
            Schweizer,M. and Nitsch,R.M.
  TITLE     Muscarinic acetylcholine receptors induce the expression of the
            immediate early growth regulatory gene CYR61
  JOURNAL   J. Biol. Chem. 275 (37), 28929-28936 (2000)
  MEDLINE   20435857
   PUBMED   10852911
REFERENCE   2  (bases 1 to 2021)
  AUTHORS   von der Kammer,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-APR-1997) H. von der Kammer, Zentrum fuer Molekulare
            Neurobiologie Hamburg, Martinistr. 52, D-20246 Hamburg, FRG
FEATURES             Location/Qualifiers
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BASE COUNT      491 a    529 c    534 g    467 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 2.5e-235;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
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Db        215 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 274

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
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Db        275 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 334

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
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Db        335 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 394

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
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Db        395 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 454

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
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Db        875 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 934

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
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Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
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Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
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Db       1175 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1234

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Qy       1141 GACTAA 1146
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Db       1355 GACTAA 1360


RESULT 8
HSCYR61M
LOCUS       HSCYR61M                2025 bp    mRNA    linear   PRI 03-FEB-1998
DEFINITION  Homo sapiens mRNA for hCYR61 protein.
ACCESSION   Z98053
VERSION     Z98053.1  GI:2832336
KEYWORDS    hCYR61 protein.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2025)
  AUTHORS   Schuetze,N., Lechner,A., Groll,C., Koehrle,J. and Jakob,F.
  TITLE     Regulation of hCYR61 by vitamin D, serum and cytokines in fetal
            human osteoblasts
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2025)
  AUTHORS   Schuetze,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1997) Klinische Forschergruppe, Medizinische
            Poliklinik, Roentgenring 11, Wuerzburg 97070, Germany
FEATURES             Location/Qualifiers
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                     /cell_line="FOB fetal osteoblasts"
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     CDS             219. .1364
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BASE COUNT      490 a    531 c    537 g    467 t
ORIGIN

  Query Match           100.0%;  Score 1146;  DB 9;  Length 2025;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-235;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
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Qy         61 CTGGCGCTCTCCACCTGCCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
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Db        279 CTGGCGCTCTCCACCTGCCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 338

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Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
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Db        399 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 458

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
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Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
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Db        519 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 578

Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
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Db        579 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 638

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Db        639 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 698

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
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Db        699 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 758

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
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Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
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Db        819 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 878

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
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Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
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Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
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Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
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Db       1299 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1358

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RESULT 9
BC016952
LOCUS       BC016952                2041 bp    mRNA    linear   PRI 09-NOV-2001
DEFINITION  Homo sapiens, clone MGC:21510 IMAGE:3886130, mRNA, complete cds.
ACCESSION   BC016952
VERSION     BC016952.1  GI:16877412
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2041)
```

```
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-NOV-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 22 Row: c Column: 20.
FEATURES              Location/Qualifiers
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                      /db_xref="taxon:9606"
                      /clone="MGC:21510 IMAGE:3886130"
                      /tissue_type="Lung, carcinoma, large cell
                      undifferentiated."
                      /clone_lib="NIH_MGC_69"
                      /lab_host="DH10B"
                      /note="Vector: pCMV-SPORT6"
     CDS              216. .1361
                      /codon_start=1
                      /product="Unknown (protein for MGC:21510)"
                      /protein_id="AAH16952.1"
                      /db_xref="GI:16877413"
                      /translation="MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVG
                      LVRDGCGCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEY
                      NSRIYQNGESFQPNCKHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEE
                      WVCDEDSIKDPMEDQDGLLGKELGFDASEVELTRNNELIAVGKGSSLKRLPVFGMEPR
                      ILYNPLQGQKCIVQTTSWSQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPV
                      YSSLKKGKKCSKTKKSPEPVRFTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMR
                      FRCEDGETFSKNVMMIQSCKCNYNCPHANEAAPFFYRLFNDIHKFRD"
BASE COUNT      509 a    529 c    535 g    468 t
ORIGIN

  Query Match           100.0%;  Score 1146;  DB 9;  Length 2041;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-235;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
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Db        216 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 275

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 335

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
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Db        336 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 395

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
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Db        396 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 455

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
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Db        456 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 515

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
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Db        516 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 575

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Db        576 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 635

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
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Db        636 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 695

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
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Db        696 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 755

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
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Db        756 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 815

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
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Db        816 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 875

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
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Db        876 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 935

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
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Db        936 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 995

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
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Db        996 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 1055

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
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Db       1056 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1115

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
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Db       1116 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1175

Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
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Db       1176 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1235

Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
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Db       1236 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1295

Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
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Db       1296 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1355

Qy       1141 GACTAA 1146
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Db       1356 GACTAA 1361


RESULT 10
BC009199
LOCUS       BC009199               2046 bp    mRNA    linear   PRI 12-JUL-2001
DEFINITION  Homo sapiens, clone MGC:15336 IMAGE:3830296, mRNA, complete cds.
ACCESSION   BC009199
VERSION     BC009199.1  GI:14327949
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2046)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
```

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  JOURNAL   Submitted (06-JUN-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
            Greene, Mark Ketteman and Anuradha Madan

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 24 Row: f Column: 2
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 2130526.
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                     /note="Vector: pOTB7"
     CDS             218. .1363
                     /codon_start=1
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                     /db_xref="GI:14327950"
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                     WVCDEDSIKDPMEDQDGLLGKELGFDASEVELTRNNELIAVGKGSSLKRLPVFGMEPR
                     ILYNPLQGQKCIVQTTSWSQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPV
                     YSSLKKGKKCSKTKKSPEPVRFTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMR
                     FRCEDGETFSKNVMMIQSCKCNYNCPHANEAAFPFYRLFNDIHKFRD"
BASE COUNT      511 a    532 c    536 g    467 t
ORIGIN

  Query Match           100.0%;  Score 1146;  DB 9;  Length 2046;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-235;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
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Db        218 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 277

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
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Db        278 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 337

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
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Db        338 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 397

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 457

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
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Db        458 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 517

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
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Db        518 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 577

Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
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Db        578 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 637

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
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Db        638 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 697

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
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Db        698 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 757

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
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Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
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Db        818 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 877

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
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Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
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Db        938 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 997

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
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Db        998 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 1057

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
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Db       1058 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1117

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
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Db       1118 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1177

Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
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Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
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Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
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Db       1298 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1357

Qy       1141 GACTAA 1146
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Db       1358 GACTAA 1363

RESULT 11
HSCYR61
LOCUS       HSCYR61                 2052 bp    mRNA    linear   PRI 16-JAN-1998
DEFINITION  H.sapiens CYR61 mRNA.
ACCESSION   Y11307
VERSION     Y11307.1  GI:2791897
KEYWORDS    cyr61 gene; cyr61 protein.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2052)
  AUTHORS   Martinerie,C., Viegas-Pequignot,E., Nguyen,V.C. and Perbal,B.
  TITLE     Chromosomal mapping and expression of the human CYR61 gene in tumor
            cells from the nervous system
  JOURNAL   J. Clin. Pathol. Mol. Pathol. 50, 130-136 (1997)
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REFERENCE   2  (bases 1 to 2052)
  AUTHORS   Perbal,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-FEB-1997) B. Perbal, Institut Curie, Centre
            Universitaire, Bat 110, 91405 Orsay Cedex, FRANCE
COMMENT     Related sequence M32490.
FEATURES             Location/Qualifiers
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BASE COUNT      499 a    542 c    543 g    468 t
ORIGIN

  Query Match             99.9%;  Score 1144.4;  DB 9;  Length 2052;
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  Matches 1145;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
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Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
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Db        284 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 343

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
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Db        344 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 403

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
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Db        404 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 463

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 523

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 583

Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
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Db        644 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 703

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
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Db        704 TGGGTCTGTGACCAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 763

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
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Db        764 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 823

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
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Db        824 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 883

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
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Db        884 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 943

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
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Db        944 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 1003

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
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Db       1004 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 1063

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
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Db       1064 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1123

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
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Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
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Db       1184 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1243

Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
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Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
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Db       1304 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1363

Qy       1141 GACTAA 1146
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RESULT 12
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LOCUS       AX206704               1418 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 3 from Patent WO0155210.
ACCESSION   AX206704
VERSION     AX206704.1  GI:15394606
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1418)
  AUTHORS   Lau,L.F., Yeung,C.Y. and Greenspan,J.A.
  TITLE     Cyr61 compositions and methods
  JOURNAL   Patent: WO 0155210-A 3 02-AUG-2001;
            Munin Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .1418
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                 ILYNPLQGQKCIVQTTSWSQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPV
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BASE COUNT      334 a    407 c    398 g    279 t
ORIGIN

  Query Match           99.7%;  Score 1142.8;  DB 6;  Length 1418;
  Best Local Similarity  99.8%;  Pred. No. 1.2e-234;
  Matches 1144;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
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Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
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Db        184 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 243

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
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Db        244 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 303

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
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Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
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Db        544 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 603

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
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Db        604 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 663

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
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Db        664 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 723

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
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Db        724 GTTGGAAAAGGCAGATCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 783

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
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Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
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Db        844 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 903

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 963

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
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Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
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Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
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Qy        1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
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Qy        1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
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Db        1204 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1263

Qy        1141 GACTAA 1146
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Db        1264 GACTAA 1269


RESULT 13
AX035239
LOCUS       AX035239                2270 bp    DNA     linear   PAT 15-NOV-2000
DEFINITION  Sequence 56 from Patent WO0053734.
ACCESSION   AX035239
VERSION     AX035239.1  GI:11190986
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2270)
  AUTHORS   Glienke,J., Hinzmann,B., Pilarsky,C. and Thierauch,K.H.
  TITLE     Human nucleic acid and protein sequences obtained from endothelial
            cells
  JOURNAL   Patent: WO 0053734-A 56 14-SEP-2000;
            SCHERING AG (DE) ; GLIENKE JENS (DE) ; HINZMANN BERND (DE) ;
            PILARSKY CHRISTIAN (DE) ; THIERAUCH KARL HEINZ (DE)
FEATURES             Location/Qualifiers
     source          1. .2270
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      590 a    561 c    577 g    542 t
ORIGIN

  Query Match           99.7%;  Score 1142.8;  DB 6;  Length 2270;
  Best Local Similarity  99.8%;  Pred. No. 1.2e-234;
  Matches 1144;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
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Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
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Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
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Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
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Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
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Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
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Db       630 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 689

Qy       481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
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Qy       661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
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Qy       781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
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Db      1110 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1169

Qy       961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
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Qy      1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
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Qy      1141 GACTAA 1146
Db      1350 GACTAA 1355
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DEFINITION  Sequence 56 from Patent EP1166798.
ACCESSION   AX342093
VERSION     AX342093.1  GI:18151661
KEYWORDS    .
SOURCE      human.
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Siemeister,G., Haberey,M. and Thierauch,K.H.
  TITLE     Combinations and compositions which interfere with vegf/vegf and
            angiopoietin/ tie receptor function and their use
  JOURNAL   Patent: EP 1166798-A 56 02-JAN-2002;
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            Schering Aktiengesellschaft (DE)
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     source          1. .2270
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                     /db_xref="taxon:9606"
BASE COUNT      590 a    561 c    577 g    542 t
ORIGIN

  Query Match           99.7%;  Score 1142.8;  DB 6;  Length 2270;
  Best Local Similarity   99.8%;  Pred. No. 1.2e-234;
  Matches 1144;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
Db       210 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 269

Qy        61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
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Qy       121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
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Qy       181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
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Qy       241 GGCGCCAGCTCCACCCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
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Qy       361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
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Qy       421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
Db       630 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 689

Qy       481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
Db       690 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 749

Qy       541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
Db       750 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 809

Qy       601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
Db       810 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 869

Qy       661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
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Qy       721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
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Qy       1141 GACTAA 1146

Db       1350 GACTAA 1355


RESULT 15
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LOCUS       AX342153               2270 bp    DNA     linear   PAT 12-JAN-2002
DEFINITION  Sequence 56 from Patent EP1166799.
ACCESSION   AX342153
VERSION     AX342153.1  GI:18151720
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Siemeister,G., Haberey,M. and Thierauch,K.H.
  TITLE     Combinations and compositions which interfere with vegf/vegf and
            angiopoietin/tie receptor function and their use (ii)
  JOURNAL   Patent: EP 1166799-A 56 02-JAN-2002;
            SCHERING AKTIENGESELLSCHAFT (DE)
FEATURES             Location/Qualifiers
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BASE COUNT      590 a    561 c    577 g    542 t
ORIGIN

  Query Match           99.7%;  Score 1142.8;  DB 6;  Length 2270;
  Best Local Similarity   99.8%;  Pred. No. 1.2e-234;
  Matches 1144;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60

Db        210 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 269

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120

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Db        390 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 449

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300

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Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420

Db        570 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 629

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480

Db        630 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 689

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540

Db        690 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 749

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600

Db        750 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 809

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660

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Db        870 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 929

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780

Db        930 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 989

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840

Db        990 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 1049

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900

Db       1050 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1109

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960

Db       1110 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1169

Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020

Db       1170 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1229

Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080

Db       1230 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1289

Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140

Db       1290 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1349

Qy       1141 GACTAA 1146

Db       1350 GACTAA 1355


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Job time : 3120 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 10, 2003, 06:16:29 ; Search time 324 Seconds
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Perfect score: 1146
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1146	100.0	1146	18	AAT97142	Human monocyte mat
2	1146	100.0	1146	24	AAD29095	Human connective t
3	1146	100.0	1418	24	ABK48899	DNA encoding human
4	1146	100.0	1419	24	ABA93130	Human Cyr61 protei
5	1146	100.0	2016	22	AAH02896	Human shear stress
6	1146	100.0	2016	24	ABQ88130	Human osteoblast d
7	1146	100.0	2016	24	ABK64742	Human benign prost
8	1146	100.0	2016	24	ABL68558	Kidney cancer rela
9	1146	100.0	2016	24	ABA93127	Human Cyr61 protei
10	1146	100.0	2021	24	ABQ88129	Human osteoblast d
11	1146	100.0	2025	24	ABQ88128	Human osteoblast d
12	1146	100.0	2307	21	AAC78196	Human cancer assoc
13	1144.4	99.9	2052	24	ABQ88127	Human osteoblast d
14	1142.8	99.7	1418	18	AAT94699	Human cysteine ric
15	1142.8	99.7	1418	22	AAD11221	Human cysteine-ric
16	1142.8	99.7	2270	21	AAA98875	Human proliferatio
17	1142.8	99.7	2270	21	AAA98157	Human proliferatio
18	1142.8	99.7	2270	24	AAD29986	Human pharmaceutic
19	1141.2	99.6	1887	24	ABQ88131	Human osteoblast d
20	1075.6	93.9	1128	17	AAT12653	Connective tissue
21	1075.6	93.9	1128	24	AAD29099	Human alternative
22	1073	93.6	1128	20	AAZ11720	Human CTGF-2 cDNA.
23	896	78.2	1480	22	AAD11220	Mouse cysteine-ric
24	896	78.2	2028	13	AAQ26421	Gene for beta-IG-M
25	513	44.8	806	22	AAH81693	Human differential
c 26	426.6	37.2	493	24	ABQ60145	Human colon cancer
27	372	32.5	372	15	AAQ57417	CYR61 like protein
28	214	18.7	255	22	AAH81876	Rat differential t
29	204.4	17.8	2075	16	AAT04226	Connective tissue
30	204.4	17.8	2075	18	AAT45360	Human connective t
31	204.4	17.8	2075	18	AAT51234	Connective tissue
32	204.4	17.8	2075	19	AAV38085	Human connective t
33	204.4	17.8	2075	20	AAX61317	Human connective t
34	204.4	17.8	2075	21	AAA11278	Human connective t
35	204.4	17.8	2075	21	AAA11280	Human connective t
36	204.4	17.8	2075	22	AAD11223	Human connective t
37	204.4	17.8	2075	22	AAF59954	Human connective t
38	204.4	17.8	2075	22	AAC87517	Human connective t
39	204.4	17.8	2075	24	ABK64553	Human benign prost
40	204.4	17.8	2312	22	AAH28213	Nucleotide sequenc
41	204.4	17.8	2312	22	AAH02914	Human shear stress
42	202.6	17.7	351	21	AAA43437	Human secreted exp
43	200	17.5	2330	13	AAQ26422	Gene for beta-IG-M
44	198.4	17.3	2267	18	AAT94700	Murine Fisp12 cDNA
45	198.4	17.3	2267	22	AAD11222	Mouse fibroblast s

ALIGNMENTS

RESULT 1
AAT97142
ID AAT97142 standard; cDNA; 1146 BP.
XX
AC AAT97142;
XX
DT 05-MAR-1998 (first entry)
XX
DE Human monocyte mature differentiation factor encoding cDNA.
XX
KW Human; monocyte; mature; differentiation factor; MMDF; macrophage;
KW cancer; immune activator; tissue culture; infectious disease; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1146
FT /*tag= a
FT /product= Monocyte_mature_differentiation_factor
XX
PN JP09234079-A.
XX
PD 09-SEP-1997.
XX
PF 04-MAR-1996; 96JP-0075236.
XX
PR 04-MAR-1996; 96JP-0075236.
XX
PA (TOYM) TOYOBO KK.
XX
DR WPI; 1997-497320/46.
DR P-PSDB; AAW35957.

XX
PT A monocyte mature differentiation factor - useful for the long term
PT tissue culture of macrophage(s)
XX
PS Claim 16; Page 13; 22pp; Japanese.
XX
CC The present sequence encodes a monocyte mature differentiation factor
CC (MMDF) which maintains the life of macrophages for long periods in
CC liquid culture. MMDF can be used as an anti-cancer agent, an immune
CC activator and to treat infectious diseases.
XX
SQ Sequence 1146 BP; 278 A; 325 C; 313 G; 230 T; 0 other;

Query Match 100.0%; Score 1146; DB 18; Length 1146;
Best Local Similarity 100.0%; Pred. No. 6.5e-301;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
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Qy         61 CTGGCGCTCTCCACCTGCCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
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Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
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Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
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Db        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360

Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
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Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
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Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
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Qy       1141 GACTAA 1146
              ||||||
Db       1141 GACTAA 1146
```

RESULT 2
AAD29095
ID AAD29095 standard; cDNA; 1146 BP.
XX
AC AAD29095;
XX
DT 07-MAY-2002 (first entry)
XX
DE Human connective tissue growth factor-2 (CTGF-2) cDNA.
XX
KW Human; angiogenesis; connective tissue growth factor-2; CTGF-2; tumour;
KW ischaemia; restenosis; tissue repair; wound healing; congenital defect;
KW cardiovascular disease; atherosclerosis; heart failure; angina; trauma;
KW burns; osteoporosis; periodontal disease; liver failure; tranquillizer;
KW vulnerary; cosmetic plastic surgery; vasotropic; hepatotropic; ulcer;
KW gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1146
FT /*tag= a
FT /product= "Human CTGF-2"
XX
PN WO200204480-A2.
XX
PD 17-JAN-2002.
XX
PF 11-JUL-2001; 2001WO-US21799.
XX
PR 11-JUL-2000; 2000US-217402P.
PR 18-MAY-2001; 2001US-291642P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (TRGE) TRANSGENE SA.
XX
PI Li H, Adams MD, Calenda V, Fataccioli V;
XX
DR WPI; 2002-171698/22.
DR P-PSDB; AAE18107.
XX
PT Stimulating angiogenesis in a mammal preferably human having ischemia
PT or restenosis or is treated for limb revascularization, by
PT administering connective tissue growth factor-2 polypeptide or
PT polynucleotide -
XX
PS Example 1; Fig 1; 131pp; English.
XX

```
CC   The present invention relates to a method for stimulating angiogenesis in
CC   a mammal. The method comprises administering a polynucleotide encoding
CC   connective tissue growth factor-2 (CTGF-2) or an active fragment or its
CC   derivative. The method is useful for stimulating angiogenesis in a mammal
CC   preferably human having ischaemia or restenosis or is treated for limb
CC   revascularisation which is leg or arm. The invention is useful for
CC   inhibiting tumour growth, where angiogenesis is utilised for enhancing
CC   the repair of connective and support tissue, promoting the attachment,
CC   fixation and stabilisation of tissue implants and enhancing wound
CC   healing, hence is useful for treating cardiovascular disease e.g.
CC   atherosclerosis, reperfusion injury such as heart failure, angina,
CC   ischaemia; and is also used to differentiate, proliferate and attract
CC   cells leading to regeneration of tissues which is utilised to repair
CC   replace or protect tissue damaged by congenital defects, trauma (burns,
CC   ulcer, etc), age, disease (e.g. osteoporosis, periodontal disease,
CC   liver failure), surgery including cosmetic plastic surgery. The present
CC   sequence is human CTGF-2 cDNA. CTGF-2 gene is useful in gene therapy.
XX
SQ   Sequence 1146 BP; 278 A; 325 C; 313 G; 230 T; 0 other;

  Query Match             100.0%;  Score 1146;  DB 24;  Length 1146;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-301;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
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Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
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Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
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Db        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960

Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020

Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080

Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140

Qy       1141 GACTAA 1146
              ||||||
Db       1141 GACTAA 1146
```

```
RESULT 3
ABK48899
ID   ABK48899 standard; DNA; 1418 BP.
XX
AC   ABK48899;
XX
DT   30-JUL-2002  (first entry)
XX
DE   DNA encoding human Cyr61.
XX
KW   Human; uterine leiomyoma proliferation; uterine leiomyoma formation;
KW   Cyr61; cytostatic; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             124..1269
FT                   /*tag= a
FT                   /product= "Cyr61"
XX
PN   WO200226193-A2.
XX
PD   04-APR-2002.
XX
PF   28-SEP-2001; 2001WO-US30783.
XX
PR   29-SEP-2000; 2000US-236887P.
XX
PA   (AMHP ) AMERICAN HOME PROD CORP.
XX
PI   Zhang Z,  Sampath D,  Zhu Y,  Winneker R;
XX
DR   WPI; 2002-383245/41.
DR   P-PSDB; AAU79761.
XX
PT   Preventing uterine leiomyoma formation or inhibiting proliferation of
PT   uterine leiomyoma in subject, comprises modulating or increasing the
PT   level of Cyr61 in leiomyoma tissue
XX
PS   Disclosure; Fig 6; 92pp; English.
XX
```

CC The present invention relates to a method of inhibiting proliferation
CC of uterine leiomyoma or preventing uterine leiomyoma formation. The
CC method comprises increasing the level of Cyr61 in leiomyoma tissue.
CC The invention also describes compounds and compositions that stimulate
CC induction of the Cyr61 gene and compounds that increase Cyr61 activity.
CC The compositions and the method of the invention are useful for
CC preventing uterine leiomyoma formation or inhibiting proliferation of
CC uterine leiomyoma in a subject. The method is particularly useful for
CC treating or preventing uterine leiomyoma formation, or inhibiting
CC proliferation of uterine leiomyoma in a subject. The present sequence
CC encodes human Cyr61.
CC Note: The present sequence shown in Fig 6 is not shown in the correct
CC sequence order in the figure. The start of the sequence is shown on
CC page 8/10 of the figures, and the rest of the sequence is shown on
CC pages 6/10 and page 7/10 of the figures.
XX
SQ Sequence 1418 BP; 334 A; 407 C; 398 G; 279 T; 0 other;

Query Match 100.0%; Score 1146; DB 24; Length 1418;
Best Local Similarity 100.0%; Pred. No. 7.1e-301;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 183

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 243

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 303

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 363

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 423

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 483

Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 543

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 603

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 663

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 723

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 783

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 843

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 903

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 GTGAAAGAAACCCGGATTTGTGAGGTGCCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 963

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1023

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1083

Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1143

Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1144 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1203

Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1204 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1263

Qy       1141 GACTAA 1146
              ||||||
Db       1264 GACTAA 1269
```

RESULT 4
ABA93130
ID ABA93130 standard; cDNA; 1419 BP.
XX
AC ABA93130;
XX
DT 15-APR-2002 (first entry)
XX
DE Human Cyr61 protein encoding cDNA.
XX
KW Human; Cyr61; breast cancer; sex steroid receptor; cytostatic; promoter;
KW sex steroid response element; cysteine rich heparin-binding protein;
KW cell proliferation; heparin binding epidermal growth factor;
KW epidermal growth factor; basic fibroblastic growth factor; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 124..1269
FT /*tag= a
FT /product= "Cyr61 protein"
XX
PN WO200198359-A2.
XX
PD 27-DEC-2001.
XX
PF 21-JUN-2001; 2001WO-US19823.
XX
PR 21-JUN-2000; 2000US-213182P.
PR 16-MAY-2001; 2001US-291510P.
XX
PA (AMHP) AMERICAN HOME PROD CORP.
XX
PI Sampath D, Zhang Z, Winneker R;
XX
DR WPI; 2002-147796/19.
DR P-PSDB; ABB05438.
XX
PT Regulation of Cyr61 expression and activity for preventing and
PT inhibiting breast cancer comprises use of a Cyr61 neutralizing
PT antibody, an anti-sense oligonucleotide and an antibody which
XX
PS Disclosure; Fig 2A-C; 86pp; English.

```
XX
CC   The present invention describes a method for the prevention or inhibition
CC   of breast cancer cell proliferation. The method comprises administration
CC   of a compound that inhibits the interaction of a sex steroid receptor
CC   with a sex steroid response element of the Cyr61 (cysteine rich heparin-
CC   binding protein) promoter. Cyr61 has cytostatic activity. An antibody (I)
CC   which neutralises Cyr61 can be used to prevent or inhibit breast cancer
CC   cell proliferation by blocking sex steroid induced and growth factor
CC   induced synthesis of Cyr61 DNA, where the growth factor is epidermal,
CC   heparin binding epidermal or basic fibroblastic growth factor. (I) can be
CC   used to diagnose or stage breast cancer where the level of Cyr61 in a
CC   positive/suspect breast cancer cell is compared to the level in a
CC   normal cell, an increase in the level of Cyr61 compared to the level in
CC   normal tissue indicates the presence of breast cancer. The level of
CC   Cyr61 being determined by exposing the tissues to (I), and an increase
CC   in the level of bound antibody by the suspect/positive cell as compared
CC   to the normal tissue indicates the presence of breast cancer. The present
CC   sequence encodes the human Cyr61 protein, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 1419 BP; 334 A; 407 C; 399 G; 279 T; 0 other;

  Query Match             100.0%;  Score 1146;  DB 24;  Length 1419;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-301;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 183

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 243

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 303

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 363

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 423

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 483

Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 543

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 603

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 663

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 723

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 783

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 843

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 903

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 963

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1023

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1083

Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1143

Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1144 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1203

Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1204 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1263

Qy       1141 GACTAA 1146
              ||||||
Db       1264 GACTAA 1269


RESULT 5
AAH02896
ID   AAH02896 standard; DNA; 2016 BP.
XX
AC   AAH02896;
XX
DT   15-JUN-2001  (first entry)
XX
DE   Human shear stress-response coding sequence SEQ ID NO: 45.
XX
KW   Human; shear stress-response protein; vascular disease;
KW   arteriosclerosis; ds.
XX
OS   Homo sapiens.
XX
PN   WO200125427-A1.
XX
PD   12-APR-2001.
XX
PF   02-OCT-2000; 2000WO-JP06840.
XX
PR   01-OCT-1999;   99JP-0280976.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
PA   (NOJI/) NOJIMA H.
XX
PI   Nojima H,  Yoshisue H,  Obayashi M,  Ota T,  Kawabata A,  Sakurada K;
PI   Kuga T,  Sekine S,  Nakamura Y,  Sugano S;
XX
DR   WPI; 2001-266308/27.
DR   P-PSDB; AAB90773.
XX
PT   DNA sequences, proteins encoded by them and antibodies against them
PT   useful in diagnosis and treatment of vascular disease caused by
PT   arteriosclerosis -
XX
PS   Claim 20; Page 341-344; 678pp; Japanese.
XX
CC   The present invention provides the protein and coding sequences of a
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```
CC   number of human shear stress response proteins. These are useful in the
CC   diagnosis, treatment and screening of vascular diseases caused by
CC   arteriosclerosis, including heart failure, post-PTCA restenosis and
CC   hypertension.
XX
SQ   Sequence 2016 BP; 490 A; 525 C; 534 G; 467 T; 0 other;

  Query Match           100.0%;  Score 1146;  DB 22;  Length 2016;
  Best Local Similarity  100.0%;  Pred. No. 8.3e-301;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 269

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 329

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 389

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 449

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 509

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 569

Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        570 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 629

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 689

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 749

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        750 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 809

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        810 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 869

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        870 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 929

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        930 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 989

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        990 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 1049

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1050 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1109

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1110 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1169

Qy         961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1170 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1229

Qy        1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1230 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1289

Qy        1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1290 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1349

Qy        1141 GACTAA 1146
               ||||||
Db       1350 GACTAA 1355


RESULT 6
ABQ88130
ID   ABQ88130 standard; cDNA; 2016 BP.
XX
AC   ABQ88130;
XX
DT   18-SEP-2002  (first entry)
XX
DE   Human osteoblast differentiation related cDNA SEQ ID NO 37.
XX
KW   Human; osteoblast; stem cell differentiation; bone tissue deposition;
KW   osteoporosis; osteopathic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200250301-A2.
XX
PD   27-JUN-2002.
XX
PF   18-DEC-2001; 2001WO-US48276.
XX
PR   18-DEC-2000; 2000US-255882P.
PR   24-APR-2001; 2001US-285691P.
XX
PA   (GENE-) GENE LOGIC INC.
PA   (PROC ) PROCTER & GAMBLE CO.
XX
PI   Ji D,  Axelrod DW,  Cook JS,  Jaiswal N,  Einstein R,  Houghton A;
PI   Mertz L;
XX
DR   WPI; 2002-557663/59.
XX
PT   Use of genes and their expression profiles associated with osteoblast
PT   differentiation for screening modulators bone formation, for diagnosing
PT   or treating e.g. osteoporosis, or as markers for the differentiation
PT   process
XX
PS   Claim 1; SEQ ID NO 37; 78pp + Sequence Listing; English.
XX
CC   The invention relates to genes and their expression profiles are used
CC   for:
CC   (a) screening modulators of precursor stem cell differentiation into
CC   osteoblasts, or bone tissue deposition;
CC   (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
CC   osteoblast formation or osteoporosis; or
CC   (c) treating or monitoring treatment of the conditions cited in (b), or
CC   monitoring the progression of bone tissue deposition.
CC   Specific conditions include postmenopausal osteoporosis, glucocorticoid
CC   osteoporosis or male osteoporosis, osteopenia, osteodystrophy,
CC   drug-induced abnormalities in bone formation or bone loss, conditions
CC   that involve altered bone metabolism (e.g. idiopathic juvenile
CC   osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
CC   Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
CC   osteoblast differentiation associated cDNA marker of the invention.
```

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CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2016 BP; 490 A; 525 C; 534 G; 467 T; 0 other;

  Query Match           100.0%;  Score 1146;  DB 24;  Length 2016;
  Best Local Similarity  100.0%;  Pred. No. 8.3e-301;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 269

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 329

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 389

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 449

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 509

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 569

Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        570 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 629

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 689

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 749

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        750 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 809

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        810 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 869

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        870 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 929

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        930 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 989

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        990 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 1049

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1050 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1109

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1110 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1169

Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1170 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1229

Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1230 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1289

Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1290 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1349

Qy       1141 GACTAA 1146
              ||||||
Db       1350 GACTAA 1355


RESULT 7
ABK64742
ID   ABK64742 standard; DNA; 2016 BP.
XX
AC   ABK64742;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human benign prostatic hyperplasia gene #637.
XX
KW   Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200212440-A2.
XX
PD   14-FEB-2002.
XX
PF   07-AUG-2001; 2001WO-US24708.
XX
PR   07-AUG-2000; 2000US-223323P.
PR   05-JUN-2001; 2001US-0873319.
XX
PA   (GENE-) GENE LOGIC INC.
PA   (NISB ) JAPAN TOBACCO INC.
XX
PI   Munger WE,  Kulkarni P,  Getzenberg RH,  Waga I,  Yamamoto J;
XX
DR   WPI; 2002-257476/30.
XX
PT   Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PT   detecting expression levels of one or more genes in prostate cells from
PT   patient that are differentially regulated compared to normal prostate
PT   cells -
XX
PS   Disclosure; Page 347; 444pp; English.
XX
CC   The invention relates to a method of diagnosing (I) the onset or
CC   progression of benign prostatic hyperplasia (BPH), or screening (II) for
CC   or identifying an agent that modulates the onset or progression of BPH.
CC   The method is based on changes in gene expression in BPH tissue isolated
CC   from patients exhibiting different clinical states of prostate
CC   hyperplasia as compared to normal prostate tissue. (I) comprises
CC   detecting the expression levels of one or more genes in prostate cells
CC   from the subject that are differentially regulated compared to normal
CC   prostate cells. (II) comprises preparing a first gene expression profile
CC   of BPH cells or BPH-like cell population, exposing the cells to the
CC   agent, preparing a second gene expression profile of the agent exposed
CC   cells, and comparing the first and second gene expression profiles.
CC   (I) is useful for diagnosing the onset or progression of BPH. (II) is
CC   useful for identifying an agent that modulates the onset or progression
CC   of BPH. The methods are useful to present information identifying
CC   the expression level in a tissue or cells, by comparing the expression
CC   level of genes given in the specification in the tissue or cells to the
CC   level of expression of gene in the database, and displaying the
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CC   expression levels of at least one gene in the tissue or cell sample
CC   compared to the expression level in BPH. Agents using (II) are useful for
CC   treating BPH or prostate cancer. ABK64106-ABK64860 represent human
CC   benign prostatic hyperplasia gene sequences of the invention.
XX
SQ   Sequence 2016 BP; 490 A; 525 C; 534 G; 467 T; 0 other;

  Query Match           100.0%;  Score 1146;  DB 24;  Length 2016;
  Best Local Similarity  100.0%;  Pred. No. 8.3e-301;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 269

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 329

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 389

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 449

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 509

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 569

Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        570 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 629

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 689

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 749

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        750 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 809

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        810 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 869

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        870 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 929

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        930 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 989

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        990 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 1049

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1050 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1109

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1110 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1169

Qy         961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1170 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1229

Qy        1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1230 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1289

Qy        1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1290 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1349

Qy        1141 GACTAA 1146
               ||||||
Db        1350 GACTAA 1355


RESULT 8
ABL68558
ID   ABL68558 standard; DNA; 2016 BP.
XX
AC   ABL68558;
XX
DT   15-MAY-2002  (first entry)
XX
DE   Kidney cancer related gene sequence SEQ ID NO:6895.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US10838.
XX
PR   05-JUN-2000; 2000US-209473P.
PR   05-JUN-2000; 2000US-209531P.
PR   18-SEP-2000; 2000US-233133P.
PR   18-SEP-2000; 2000US-233617P.
PR   20-SEP-2000; 2000US-234009P.
PR   20-SEP-2000; 2000US-234034P.
PR   20-SEP-2000; 2000US-234052P.
PR   22-SEP-2000; 2000US-234509P.
PR   22-SEP-2000; 2000US-234567P.
PR   25-SEP-2000; 2000US-234923P.
PR   25-SEP-2000; 2000US-234924P.
PR   25-SEP-2000; 2000US-235077P.
PR   25-SEP-2000; 2000US-235082P.
PR   25-SEP-2000; 2000US-235134P.
PR   25-SEP-2000; 2000US-235280P.
PR   26-SEP-2000; 2000US-235637P.
PR   26-SEP-2000; 2000US-235638P.
PR   27-SEP-2000; 2000US-235711P.
PR   27-SEP-2000; 2000US-235720P.
PR   27-SEP-2000; 2000US-235840P.
PR   27-SEP-2000; 2000US-235863P.
PR   28-SEP-2000; 2000US-236028P.
PR   28-SEP-2000; 2000US-236032P.
PR   28-SEP-2000; 2000US-236033P.
PR   28-SEP-2000; 2000US-236034P.
PR   28-SEP-2000; 2000US-236109P.
PR   28-SEP-2000; 2000US-236111P.
PR   29-SEP-2000; 2000US-236842P.
PR   29-SEP-2000; 2000US-236891P.
PR   02-OCT-2000; 2000US-237172P.
PR   02-OCT-2000; 2000US-237173P.
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PR   02-OCT-2000; 2000US-237278P.
PR   02-OCT-2000; 2000US-237294P.
PR   02-OCT-2000; 2000US-237295P.
PR   02-OCT-2000; 2000US-237316P.
PR   03-OCT-2000; 2000US-237425P.
PR   03-OCT-2000; 2000US-237598P.
PR   03-OCT-2000; 2000US-237604P.
PR   03-OCT-2000; 2000US-237606P.
PR   03-OCT-2000; 2000US-237608P.
PR   01-NOV-2000; 2000US-244867P.
PR   01-NOV-2000; 2000US-245084P.
XX
PA   (AVAL-) AVALON PHARM.
XX
PI   Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI   Soppet DR, Weaver Z;
XX
DR   WPI; 2002-188264/24.
XX
PT   Screening for anti-neoplastic agent involves exposing cells to a
PT   chemical agent to be tested for anti-neoplastic activity, and
PT   determining a change in expression of a gene of a signature gene set
XX
PS   Claim 1; SEQ ID 6895; 44pp; English.
XX
CC   The present invention describes a method (M1) for screening for an
CC   anti-neoplastic agent. The method involves exposing cells to a chemical
CC   agent to be tested for anti-neoplastic activity, determining a change in
CC   expression of at least one gene (I) of a signature gene set, where (I)
CC   comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC   to ABL70110), or is at least 95% identical to (S), where a change in
CC   expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC   activity and can be used in gene therapy. M1 can be used for screening
CC   an anti-neoplastic agent, and can be used for producing a product which
CC   is the data collected with respect to the anti-neoplastic agent as a
CC   result of M1, and the data is sufficient to convey the chemical
CC   structure and/or properties of the agent. M1 can be used in the
CC   treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC   oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC   adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC   infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC   carcinoma, papillary carcinoma and Wilm's tumour.
XX
SQ   Sequence 2016 BP; 490 A; 525 C; 534 G; 467 T; 0 other;

  Query Match             100.0%;  Score 1146;  DB 24;  Length 2016;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-301;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 269

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 329

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 389

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 449

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 509

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 569

Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        570 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 629

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 689

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 749

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
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Db        750 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 809

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
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Db        810 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 869

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        870 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 929

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        930 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 989

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        990 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 1049

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1050 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1109

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1110 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1169

Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1170 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1229

Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1230 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1289

Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1290 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1349

Qy       1141 GACTAA 1146
              ||||||
Db       1350 GACTAA 1355


RESULT 9
ABA93127
ID   ABA93127 standard; cDNA; 2016 BP.
XX
AC   ABA93127;
XX
DT   15-APR-2002  (first entry)
XX
DE   Human Cyr61 protein encoding cDNA SEQ ID NO:1.
XX
KW   Human; Cyr61; breast cancer; sex steroid receptor; cytostatic; promoter;
KW   sex steroid response element; cysteine rich heparin-binding protein;
KW   cell proliferation; heparin binding epidermal growth factor;
KW   epidermal growth factor; basic fibroblastic growth factor; gene; ss.
XX
OS   Homo sapiens.
```

```
XX
FH   Key             Location/Qualifiers
FT   CDS             210..1355
FT                   /*tag= a
FT                   /product= "Cyr61 protein"
XX
PN   WO200198359-A2.
XX
PD   27-DEC-2001.
XX
PF   21-JUN-2001; 2001WO-US19823.
XX
PR   21-JUN-2000; 2000US-213182P.
PR   16-MAY-2001; 2001US-291510P.
XX
PA   (AMHP ) AMERICAN HOME PROD CORP.
XX
PI   Sampath D,  Zhang Z,  Winneker R;
XX
DR   WPI; 2002-147796/19.
DR   P-PSDB; ABB05438.
XX
PT   Regulation of Cyr61 expression and activity for preventing and
PT   inhibiting breast cancer comprises use of a Cyr61 neutralizing
PT   antibody, an anti-sense oligonucleotide and an antibody which -
XX
PS   Disclosure; Page 84-85; 86pp; English.
XX
CC   The present invention describes a method for the prevention or inhibition
CC   of breast cancer cell proliferation. The method comprises administration
CC   of a compound that inhibits the interaction of a sex steroid receptor
CC   with a sex steroid response element of the Cyr61 (cysteine rich heparin-
CC   binding protein) promoter. Cyr61 has cytostatic activity. An antibody (I)
CC   which neutralises Cyr61 can be used to prevent or inhibit breast cancer
CC   cell proliferation by blocking sex steroid induced and growth factor
CC   induced synthesis of Cyr61 DNA, where the growth factor is epidermal,
CC   heparin binding epidermal or basic fibroblastic growth factor. (I) can be
CC   used to diagnose or stage breast cancer where the level of Cyr61 in a
CC   positive/suspect breast cancer cell is compared to the level in a
CC   normal cell, an increase in the level of Cyr61 compared to the level in
CC   normal tissue indicates the presence of breast cancer. The level of
CC   Cyr61 being determined by exposing the tissues to (I), and an increase
CC   in the level of bound antibody by the suspect/positive cell as compared
CC   to the normal tissue indicates the presence of breast cancer. The present
CC   sequence encodes the human Cyr61 protein, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 2016 BP; 490 A; 525 C; 534 G; 467 T; 0 other;

  Query Match             100.0%;  Score 1146;  DB 24;  Length 2016;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-301;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 269

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 329

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 389

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 449

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 509

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 569

Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        570 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 629

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 689

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 749

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        750 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 809

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        810 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 869

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        870 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 929

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        930 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 989

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        990 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 1049

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
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Db       1050 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1109

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1110 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1169

Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1170 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1229

Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1230 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1289

Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1290 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1349

Qy       1141 GACTAA 1146
              ||||||
Db       1350 GACTAA 1355


RESULT 10
ABQ88129
ID   ABQ88129 standard; cDNA; 2021 BP.
XX
AC   ABQ88129;
XX
DT   18-SEP-2002  (first entry)
XX
DE   Human osteoblast differentiation related cDNA SEQ ID NO 36.
XX
KW   Human; osteoblast; stem cell differentiation; bone tissue deposition;
KW   osteoporosis; osteopathic; ss.
```

```
XX
OS   Homo sapiens.
XX
PN   WO200250301-A2.
XX
PD   27-JUN-2002.
XX
PF   18-DEC-2001; 2001WO-US48276.
XX
PR   18-DEC-2000; 2000US-255882P.
PR   24-APR-2001; 2001US-285691P.
XX
PA   (GENE-) GENE LOGIC INC.
PA   (PROC ) PROCTER & GAMBLE CO.
XX
PI   Ji D,  Axelrod DW,  Cook JS,  Jaiswal N,  Einstein R,  Houghton A;
PI   Mertz L;
XX
DR   WPI; 2002-557663/59.
XX
PT   Use of genes and their expression profiles associated with osteoblast
PT   differentiation for screening modulators bone formation, for diagnosing
PT   or treating e.g. osteoporosis, or as markers for the differentiation
PT   process -
XX
PS   Claim 1; SEQ ID NO 36; 78pp + Sequence Listing; English.
XX
CC   The invention relates to genes and their expression profiles are used
CC   for:
CC   (a) screening modulators of precursor stem cell differentiation into
CC   osteoblasts, or bone tissue deposition;
CC   (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
CC   osteoblast formation or osteoporosis; or
CC   (c) treating or monitoring treatment of the conditions cited in (b), or
CC   monitoring the progression of bone tissue deposition.
CC   Specific conditions include postmenopausal osteoporosis, glucocorticoid
CC   osteoporosis or male osteoporosis, osteopenia, osteodystrophy,
CC   drug-induced abnormalities in bone formation or bone loss, conditions
CC   that involve altered bone metabolism (e.g. idiopathic juvenile
CC   osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
CC   Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
CC   osteoblast differentiation associated cDNA marker of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2021 BP; 491 A; 529 C; 534 G; 467 T; 0 other;

  Query Match             100.0%;  Score 1146;  DB 24;  Length 2021;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-301;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 274

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 334

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 394

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 454

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
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Db        455 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 514

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 574

Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 634

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 694

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 754

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGCAGTTCACGAGAAACAATGAATTGATTGCA 600
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Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
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Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        875 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 934

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        935 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 994

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        995 GTGAAAGAAACCCGGATTTGTGAGGTCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 1054

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1055 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1114

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1115 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1174

Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1175 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1234

Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1235 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1294

Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1295 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1354

Qy       1141 GACTAA 1146
              ||||||
Db       1355 GACTAA 1360


RESULT 11
ABQ88128
ID   ABQ88128 standard; cDNA; 2025 BP.
XX
AC   ABQ88128;.
XX
DT   18-SEP-2002  (first entry)
XX
DE   Human osteoblast differentiation related cDNA SEQ ID NO 35.
XX
KW   Human; osteoblast; stem cell differentiation; bone tissue deposition;
KW   osteoporosis; osteopathic; ss.
XX
```

```
OS   Homo sapiens.
XX
PN   WO200250301-A2.
XX
PD   27-JUN-2002.
XX
PF   18-DEC-2001; 2001WO-US48276.
XX
PR   18-DEC-2000; 2000US-255882P.
PR   24-APR-2001; 2001US-285691P.
XX
PA   (GENE-) GENE LOGIC INC.
PA   (PROC ) PROCTER & GAMBLE CO.
XX
PI   Ji D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
PI   Mertz L;
XX
DR   WPI; 2002-557663/59.
XX
PT   Use of genes and their expression profiles associated with osteoblast
PT   differentiation for screening modulators bone formation, for diagnosing
PT   or treating e.g. osteoporosis, or as markers for the differentiation
PT   process -
XX
PS   Claim 1; SEQ ID NO 35; 78pp + Sequence Listing; English.
XX
CC   The invention relates to genes and their expression profiles are used
CC   for:
CC   (a) screening modulators of precursor stem cell differentiation into
CC   osteoblasts, or bone tissue deposition;
CC   (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
CC   osteoblast formation or osteoporosis; or
CC   (c) treating or monitoring treatment of the conditions cited in (b), or
CC   monitoring the progression of bone tissue deposition.
CC   Specific conditions include postmenopausal osteoporosis, glucocorticoid
CC   osteoporosis or male osteoporosis, osteopenia, osteodystrophy,
CC   drug-induced abnormalities in bone formation or bone loss, conditions
CC   that involve altered bone metabolism (e.g. idiopathic juvenile
CC   osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
CC   Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
CC   osteoblast differentiation associated cDNA marker of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2025 BP; 490 A; 531 C; 537 G; 467 T; 0 other;

  Query Match           100.0%;  Score 1146;  DB 24;  Length 2025;
  Best Local Similarity  100.0%;  Pred. No. 8.3e-301;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 278

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 338

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 398

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 458

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 518

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        519 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 578

Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 638

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 698

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 758

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 818

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 878

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 938

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 998

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 1058

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1118

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1119 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1178

Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1238

Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1298

Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1358

Qy       1141 GACTAA 1146
              ||||||
Db       1359 GACTAA 1364


RESULT 12
AAC78196
ID   AAC78196 standard; cDNA; 2307 BP.
XX
AC   AAC78196;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human cancer associated gene sequence SEQ ID NO:590.
XX
KW   Human; cancer associated gene; cancer antigen; detection; cancer;
KW   diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;
KW   antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
KW   antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
```

```
KW   dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW   vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW   immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW   allergic reaction; graft versus host disease; organ rejection;
KW   haemostatic; thrombolytic; cardiovascular disorder; infection;
KW   neurological disease; drug screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055350-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US05882.
XX
PR   12-MAR-1999;   99US-0124270.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-587533/55.
DR   P-PSDB; AAB43987.
XX
PT   Novel isolated nucleic acids comprising sequences encoding peptides
PT   useful for treating or diagnosing e.g. cancer -
XX
PS   Claim 1; Page 1112; 2352pp; English.
XX
CC   AAC77607 to AAC78448 encode the human cancer associated proteins given
CC   in AAB43398 to AAB44239. The proteins can have activities based on the
CC   tissues and cells the genes are expressed in. Example of activities
CC   include: cytostatic; proliferative; vulnerary; immunomodulator;
CC   antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
CC   antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC   dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC   nootropic; vasotropic; antipsoriatic and antiangiogenic. The
CC   polynucleotides and polypeptides can be used for preventing, treating or
CC   ameliorating medical conditions and diagnosing pathological conditions.
CC   Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC   the present invention may be used to treat immune disorders by activating
CC   or inhibiting the proliferation, differentiation or mobilisation of
CC   immune cells, to treat disorders of haematopoietic cells, autoimmune
CC   disorders, allergic reactions, graft versus host disease and organ
CC   rejection, modulate haemostatic or thrombolytic activity, modulate
CC   inflammation, cancers, cardiovascular disorders, neurological disease and
CC   bacterial or viral infections. The peptides, nucleotides, antibodies,
CC   agonists and antagonists may be also be used in drug screens. AAC78449 to
CC   AAC78457 and AAB44240 represent sequences used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 2307 BP; 610 A; 573 C; 580 G; 544 T; 0 other;

  Query Match           100.0%;  Score 1146;  DB 21;  Length 2307;
  Best Local Similarity  100.0%;  Pred. No. 8.8e-301;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 282

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 342

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 402

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 462

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 522

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 582

Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 642

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 702

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        703 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 762

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        763 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 822

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        823 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 882

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        883 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 942

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 1002

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 1062

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1122

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1182

Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1242

Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1243 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1302

Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1362

Qy       1141 GACTAA 1146
              ||||||
Db       1363 GACTAA 1368


RESULT 13
ABQ88127
ID   ABQ88127 standard; cDNA; 2052 BP.
XX
AC   ABQ88127;
XX
DT   18-SEP-2002  (first entry)
XX
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```
DE   Human osteoblast differentiation related cDNA SEQ ID NO 34.
XX
KW   Human; osteoblast; stem cell differentiation; bone tissue deposition;
KW   osteoporosis; osteopathic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200250301-A2.
XX
PD   27-JUN-2002.
XX
PF   18-DEC-2001; 2001WO-US48276.
XX
PR   18-DEC-2000; 2000US-255882P.
PR   24-APR-2001; 2001US-285691P.
XX
PA   (GENE-) GENE LOGIC INC.
PA   (PROC ) PROCTER & GAMBLE CO.
XX
PI   Ji D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
PI   Mertz L;
XX
DR   WPI; 2002-557663/59.
XX
PT   Use of genes and their expression profiles associated with osteoblast
PT   differentiation for screening modulators bone formation, for diagnosing
PT   or treating e.g. osteoporosis, or as markers for the differentiation
PT   process -
XX
PS   Claim 1; SEQ ID NO 34; 78pp + Sequence Listing; English.
XX
CC   The invention relates to genes and their expression profiles are used
CC   for:
CC   (a) screening modulators of precursor stem cell differentiation into
CC   osteoblasts, or bone tissue deposition;
CC   (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
CC   osteoblast formation or osteoporosis; or
CC   (c) treating or monitoring treatment of the conditions cited in (b), or
CC   monitoring the progression of bone tissue deposition.
CC   Specific conditions include postmenopausal osteoporosis, glucocorticoid
CC   osteoporosis or male osteoporosis, osteopenia, osteodystrophy,
CC   drug-induced abnormalities in bone formation or bone loss, conditions
CC   that involve altered bone metabolism (e.g. idiopathic juvenile
CC   osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
CC   Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
CC   osteoblast differentiation associated cDNA marker of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2052 BP; 499 A; 542 C; 543 G; 468 T; 0 other;

  Query Match           99.9%;  Score 1144.4;  DB 24;  Length 2052;
  Best Local Similarity  99.9%;  Pred. No. 2.3e-300;
  Matches 1145;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 283

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 343

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 403

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 463

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 523

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 583

Qy        361 TGCACATGTATTGATGGCGCCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 643

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        644 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 703

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 TGGGTCTGTGACCAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 763

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        764 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 823

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        824 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 883

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        884 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 943

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        944 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 1003

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 1063

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1123

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1183

Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1184 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1243

Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1244 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1303

Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1304 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1363

Qy       1141 GACTAA 1146
              ||||||
Db       1364 GACTAA 1369

RESULT 14
AAT94699
ID   AAT94699 standard; cDNA; 1418 BP.
XX
AC   AAT94699;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Human cysteine rich protein 61 (Cyr61) cDNA.
```

```
XX
KW   Cysteine rich protein 61; Cyr61; human;
KW   extracellular matrix signalling molecule; cell adhesion;
KW   cell migration; cell proliferation; angiogenesis; chondrogenesis;
KW   oncogenesis; haematostasis; wound healing; organ regeneration; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             124..1269
FT                   /*tag= a
XX
PN   WO9733995-A2.
XX
PD   18-SEP-1997.
XX
PF   14-MAR-1997;    97WO-US04193.
XX
PR   15-MAR-1996;    96US-0013958.
XX
PA   (MUNI-) MUNIN CORP.
XX
PI   Lau LF;
XX
DR   WPI; 1997-470875/43.
DR   P-PSDB; AAW35730.
XX
PT   Isolated and purified cysteine rich protein 61, Cyr61 - useful to
PT   modulate e.g. haematostasis, induce wound healing, promote organ
PT   regeneration etc
XX
PS   Claim 14; Page 110-112; 133pp; English.
XX
CC   This cDNA clone codes for human cysteine rich protein 61 (Cyr61)
CC   (see AAW35760), an extracellular matrix signalling molecule.  It was
CC   isolated from a human placental cDNA library using as probe a
CC   partial clone obtained by PCR amplification using primers (see
CC   AAT94701-02) based on conserved regions of murine Cyr61.  Cyr61
CC   polynucleotides can be used for the production of Cyr61 by
CC   recombinant methods and as hybridisation probes.  Cyr61 can be
CC   used to modulate haematostasis, induce wound healing in a tissue,
CC   promote organ regeneration, improve tissue grafting or promote
CC   bone or prothesis implantation (claimed).  It can also be used to
CC   screen for a modulator of angiogenesis, chondrogenesis,
CC   oncogenesis, cell adhesion, cell migration, cell proliferation,
CC   expand a population of undifferentiated haematopoietic stem cells
CC   in culture and to screen for a mitogen (claimed).  Knowledge of the
CC   Cyr61 coding sequence provides the basis for the design of gene
CC   therapy approaches.
XX
SQ   Sequence 1418 BP; 334 A; 407 C; 398 G; 279 T; 0 other;

  Query Match           99.7%;  Score 1142.8;  DB 18;  Length 1418;
  Best Local Similarity  99.8%;  Pred. No. 5.2e-300;
  Matches 1144;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
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Db        124 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 183

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
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Db        184 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 243

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 303

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 363

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 423

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        424 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTCAACATCAG 483

Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 543

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 603

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
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Db        604 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 663

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
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Db        664 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 723

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        724 GTTGGAAAAGGCAGATCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 783

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
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Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
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Db        844 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 903

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
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Db        904 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 963

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
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Db        964 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1023

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1083

Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1143

Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1144 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1203

Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1204 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1263

Qy       1141 GACTAA 1146
              ||||||
Db       1264 GACTAA 1269


RESULT 15
AAD11221
ID   AAD11221 standard; cDNA; 1418 BP.
XX
AC   AAD11221;
XX
DT   24-SEP-2001  (first entry)
XX
DE   Human cysteine-rich protein (Cyr61) cDNA.
```

```
XX
KW   Cysteine-rich protein; Cyr61; extracellular matrix signalling molecule;
KW   fibroblast secreted protein; Fisp12; connective tissue growth factor;
KW   CTGF; ECM; cell adhesion; cell migration; fibroblast cell proliferation;
KW   angiogenesis; wound healing; integrin receptor; atherosclerosis; tumour;
KW   heart disease; fibrosis; gene therapy; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             124..1269
FT                   /*tag= a
FT                   /product= "Human Cyr61 protein"
XX
PN   WO200155210-A2.
XX
PD   02-AUG-2001.
XX
PF   31-JAN-2001; 2001WO-US03267.
XX
PR   31-JAN-2000; 2000US-0495448.
PR   15-MAY-2000; 2000US-0204364.
PR   06-OCT-2000; 2000US-0238705.
XX
PA   (MUNI-) MUNIN CORP.
XX
PI   Lau LF,  Yeung C,  Greenspan JA;
XX
DR   WPI; 2001-465561/50.
DR   P-PSDB; AAE05921.
XX
PT   Novel human cysteine-rich protein 61 (Cyr61) fragment useful in methods
PT   for screening for modulators of cell adhesion, fibroblast cell
PT   proliferation, angiogenesis and cell migration
XX
PS   Example 1; Page 169-171; 186pp; English.
XX
CC   The invention relates to extracellular matrix (ECM) signalling
CC   molecules involved in cellular response to growth factors. More
CC   particularly the invention is directed to cysteine-rich protein
CC   (Cyr61), and Cyr61-related proteins such as fibroblast secreted
CC   protein (Fisp12) and connective tissue growth factor (CTGF) and
CC   nucleic acid molecules encoding such proteins. The polypeptides
CC   of the invention are members of cysteine-rich secreted protein
CC   family. Human Cyr61 fragment is useful in methods for screening
CC   modulators of cell adhesion, cell migration, fibroblast cell
CC   proliferation, angiogenesis, wound healing and Cyr61-integrin
CC   receptor interaction. Modulator of Cyr61-integrin alphaVbeta3
CC   interaction is used for the preparation of a medicament for the
CC   treatment of atherosclerosis, heart disease, tumour metastasis,
CC   fibrosis, tumour growth, disorders associated with inadequate
CC   angiogenesis; aberrant granulation tissue development; aberrant
CC   fibroblast growth and wounds. Polynucleotides of the invention
CC   are useful in gene therapy. The present sequence is a cDNA
CC   encoding human Cyr61 protein.
XX
SQ   Sequence 1418 BP; 334 A; 407 C; 398 G; 279 T; 0 other;

  Query Match           99.7%;  Score 1142.8;  DB 22;  Length 1418;
  Best Local Similarity  99.8%;  Pred. No. 5.2e-300;
  Matches 1144;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 183

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 243

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 303

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 363

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
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Db        364 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 423

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
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Db        424 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTCAACATCAG 483

Qy        361 TGCACATGTATTGATGGCGCCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 TGCACATGTATTGATGGCGCCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 543

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 603

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 663

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 723

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        724 GTTGGAAAAGGCAGATCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 783

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 843

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 903

Qy        781 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 963

Qy        841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 1023

Qy        901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 1083

Qy        961 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG 1143

Qy       1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1080
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Db       1144 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG 1203

Qy       1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
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Db       1204 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1263

Qy       1141 GACTAA 1146
              ||||||
Db       1264 GACTAA 1269


Search completed: July 10, 2003, 09:20:08
Job time : 336 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 10, 2003, 06:16:29 ; Search time 1897 Seconds
(without alignments)
9783.884 Million cell updates/sec

Title: US-09-901-910-1
Perfect score: 1146
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: em_estba:*
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6: em_estpl:*
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9: gb_est1:*
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12: gb_est3:*
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14: gb_est5:*
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16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
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21: em_gss_vrt:*
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24: em_gss_mus:*
25: em_gss_other:*
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27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	894.4	78.0	2029	11	BC003205	BC003205 Mus muscu
	2	876.8	76.5	919	14	BQ925203	BQ925203 AGENCOURT
	3	807.6	70.5	895	14	BQ880408	BQ880408 AGENCOURT
	4	797.6	69.6	866	14	BQ222696	BQ222696 AGENCOURT
	5	769.6	67.2	939	14	BQ644239	BQ644239 AGENCOURT
	6	762.4	66.5	985	9	AL550072	AL550072 AL550072
	7	756.2	66.0	876	14	BQ716204	BQ716204 AGENCOURT
	8	751.6	65.6	992	14	BQ644666	BQ644666 AGENCOURT
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	10	748.8	65.3	1009	9	AL513570	AL513570 AL513570
	11	746	65.1	836	14	BQ716992	BQ716992 AGENCOURT
	12	738.6	64.5	908	14	BQ720988	BQ720988 AGENCOURT
	13	726	63.4	896	14	BQ719732	BQ719732 AGENCOURT
	14	722.6	63.1	929	9	AL541592	AL541592 AL541592
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	41	593.6	51.8	611	10	AW580842	AW580842 PM3-LT003
c	42	593.4	51.8	641	10	AW580835	AW580835 PM3-LT003
c	43	592	51.7	628	10	AW580963	AW580963 PM3-LT003
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c	45	587.6	51.3	613	10	AW580928	AW580928 PM3-LT003

ALIGNMENTS

RESULT 1
BC003205
LOCUS BC003205 2029 bp mRNA linear HTC 07-AUG-2002
DEFINITION Mus musculus, cysteine rich protein 61, clone IMAGE:3587352, mRNA.
ACCESSION BC003205
VERSION BC003205.1 GI:14707674
KEYWORDS HTC.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2029)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 10 Row: o Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein
This clone has the following problem: frame shifted.

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                     /db_xref="taxon:10090"
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                     /clone="IMAGE:3587352"
                     /tissue_type="Mammary tumor metastatized to lung. Tumor
                     arose spontaneously from a senescent normal mammary
                     (clonal) outgrowth infected with the virus MMTV."
                     /clone_lib="NCI_CGAP_Lu29"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
BASE COUNT      520 a    530 c    525 g    454 t
ORIGIN

  Query Match           78.0%;  Score 894.4;  DB 11;  Length 2029;
  Best Local Similarity   87.5%;  Pred. No. 4.3e-237;
  Matches 1008;  Conservative    0;  Mismatches  126;  Indels   18;  Gaps    2;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
              ||||||||| ||| | |||| ||||||| | | ||||||||||||||||||||||||
Db        179 ATGAGCTCCAGCACCTTCAGGACGCTCGCTGTCGGCCGTCACCCTTCTCCACTTGACCAGA 238

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
              |||||||||||||||||||||||| ||||||||||||| |||||||| ||||||||||
Db        239 CTGGCGCTCTCCACCTGCCCCGCCGCCTGCCACTGCCCTCTGGAGGCACCCAAGTGCGCC 298

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
              |||||||||| |||||||||||||||||||||||||||||||||||||| || || |||
Db        299 CCGGGAGTCGGGTTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCTAAACAACTC 358

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
              |||||||||||||||||| |||||||||||||||||||||||||| |||||||||| |||
Db        359 AACGAGGACTGCAGCAAAACTCAGCCCTGCGACCACACCAAGGGGTTGGAATGCAATTTC 418

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
              |||||||||||||||||||||||||||||||||||||||||||| ||| ||||||||||
Db        419 GGCGCCAGCTCCACCGCTCTGAAAGGGATCTGCAGAGCTCAGTGAGAAGGCAGACCCTGT 478

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        479 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGCTTCCAGCCCAACTGTAAACACCAG 538

Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        539 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTGTCTCTC 598

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
              |||||  |||||||||||||||||| ||||||| ||||| | |||||||||||| || |||
Db        599 CCCAATCTGGGCTGTCCCAACCCCCGGCTGGTGAAAGTCAGCGGGCAGTGCTGTGAAGAG 658

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
              ||||| ||||| || || || || |||||| || |||| |||||||| | ||||
Db        659 TGGGTTTGTGATGAAGACAGCATTAAGGACTCCCTGGACGACCAGGATGACCTC------ 712

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
                  || ||| |||||||||| |||||||||| |||||||||||||| || || |||
Db        713 ------CTCGGACTCGATGCCTCGGAGGTGGAGTTAACGAGAAACAATGAGTTAATCGCA 766

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
              |||||||||||||||||||||||| |||| ||||| ||||| |  || || ||  | ||
Db        767 ATTGGAAAAGGCAGCTCACTGAAGAGGCTTCCTGTCTTTGGCACCGAACCGCGAGTTCTT 826

Qy        661 TACAACCCTTT------ACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAG 714
              | ||||||| |       || |||||||||| || ||||| || || || |||||||||
Db        827 TTCAACCCTCTGCACGCCCATGGCCAGAAATGCATCGTTCAGACCACGTCCTGGTCCCAG 886

Qy        715 TGCTCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGC 774
              ||||| |||| ||| |||||||| |||||||||||||||||||||||||||||| ||||||
Db        887 TGCTCCAAGAGCTGCGGAACTGGCATCTCCACACGAGTTACCAATGACAACCCAGAGTGC 946

Qy        775 CGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGC 834
              ||||| |||||||| |||||||| ||||| ||||| |||||||||||| ||||||||||
Db        947 CGCCTGGTGAAAGAGACCCGGATCTGTGAAGTGCGTCCTTGTGGACAACCAGTGTACAGC 1006

Qy        835 AGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTT 894
              ||||| |||||||||||||||||||||||||||||||||||||| |||||||||| |||
Db       1007 AGCCTAAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCAGAACCAGTCAGATTT 1066

Qy        895 ACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTG 954
              ||||| || ||||| | ||||| |||||||||||||||| |||||||| ||||||||
Db       1067 ACTTATGCAGGATGCTCCAGTGTCAAGAAATACCGGCCCAAATACTGCGGCTCCTGCGTA 1126

Qy        955 GACGGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAA 1014
              || ||||| |||||||| || | || |||||| ||||||||||||||||||||| ||||||
Db       1127 GATGGCCGGTGCTGCACACCTCTGCAGACCAGAACTGTGAAGATGCGGTTCCGATGCGAA 1186

Qy        1015 GATGGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAAC 1074
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Db        1187 GATGGAGAGATGTTTTCCAAGAATGTCATGATGATCCAGTCCTGCAAATGTAACTACAAC 1246

Qy        1075 TGCCCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAA 1134
               ||||||||| |||| || ||| |||| |   | ||||| || ||||||||||| |||||
Db        1247 TGCCCGCATCCCAACGAGGCATCGTTCCGACTGTACAGCCTATTCAATGACATCCACAAG 1306

Qy        1135 TTTAGGGACTAA 1146
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Db        1307 TTCAGGGACTAA 1318
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RESULT 2
BQ925203
LOCUS       BQ925203                 919 bp    mRNA    linear   EST 20-AUG-2002
DEFINITION  AGENCOURT_8840401 Lupski_sciatic_nerve Homo sapiens cDNA clone
            IMAGE:6205236 5', mRNA sequence.
ACCESSION   BQ925203
VERSION     BQ925203.1  GI:22340234
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 919)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13627  row: m  column: 13
            High quality sequence stop: 658.
FEATURES             Location/Qualifiers
     source          1. .919
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                     /clone="IMAGE:6205236"
                     /clone_lib="Lupski_sciatic_nerve"
                     /sex="male"
                     /tissue_type="sciatic nerve"
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                     /dev_stage="adult, 70 yr"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.87 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."
BASE COUNT      241 a    238 c    244 g    196 t
ORIGIN

  Query Match           76.5%;  Score 876.8;  DB 14;  Length 919;
  Best Local Similarity   99.0%;  Pred. No. 2.1e-232;
  Matches  903;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    2;

Qy        235 AACTTCGGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGA 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AACTTCGGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGA 60

Qy        295 CCCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAA 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAA 120

Qy        355 CATCAGTGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTA 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATCAGTGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTA 180

Qy        415 TCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGC 474
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGC 240

Qy        475 GAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTC 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTC 300

Qy        535 CTTGGCAAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTG 594
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTGGCAAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTG 360

Qy        595 ATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGC 654
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGC 420

Qy        655 ATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAG 714
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAG 480

Qy        715 TGCTCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGC 774
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Db        481 TGCTCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGC 540

Qy        775 CGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGC 834
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Db        541 CGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGC 600

Qy        835 AGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTT 894
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTT 660

Qy        895 ACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTG 954
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTG 720

Qy        955 GACGGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAA 1014
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        721 GACGGCCGATGCTGCACGCCCCAGCTGAACAGGACTGTGAAGATGCGGTTCCGCTGCGAA 780

Qy       1015 GATGGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAAC 1074
              |||||||||| ||||||| | ||||||||||||||||||||||||||||||||||| ||
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Db         781 GATGGGGAGA-ATTTTCCCAAGACGTCATGATGATCCAGTCCTGCAAATGCAACTAC-AC 838

Qy        1075 TGCCCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAA 1134
               || ||||||| |||||||||||||||||| ||||||||||||||||||||||||||||||
Db         839 TGGCCGCATGGCAATGAAGCAGCGTTTCCCCTCTACAGGCTGTTCAATGACATTCACAAA 898

Qy        1135 TTTAGGGACTAA 1146
               ||||||||||||
Db         899 TTTAGGGACTAA 910


RESULT 3
BQ880408
LOCUS       BQ880408                 895 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8118497 Lupski_dorsal_root_ganglion Homo sapiens cDNA
            clone IMAGE:6181343 5', mRNA sequence.
ACCESSION   BQ880408
VERSION     BQ880408.1  GI:22272416
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 895)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13565  row: i  column: 24
            High quality sequence stop: 660.
FEATURES             Location/Qualifiers
     source          1. .895
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6181343"
                     /clone_lib="Lupski_dorsal_root_ganglion"
                     /sex="male"
                     /tissue_type="dorsal root ganglia"
                     /dev_stage="adult, 36 yr"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.7 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."
BASE COUNT      229 a    236 c    251 g    179 t
ORIGIN

  Query Match           70.5%;  Score 807.6;  DB 14;  Length 895;
  Best Local Similarity   97.8%;  Pred. No. 3.6e-213;
  Matches  851;  Conservative    0;  Mismatches   14;  Indels    5;  Gaps    3;

Qy        132 GCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTCAACGAGGACTG 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTCAACGAGGACTG 60

Qy        192 CAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTCGGCGCCAGCTC 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTCGGCGCCAGCTC 120
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Qy        252 CACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTC 311
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Db        121 CACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTC 180

Qy        312 CAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTAT 371
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Qy        372 TGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGG 431
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Qy        432 CTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGA 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGA 360

Qy        492 CGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGG 551
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Db        361 CGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGG 420

Qy        552 ATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGG 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGG 480

Qy        612 CAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTATACAACCCTTT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        672 ACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGG 731
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Db        541 ACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGG 600

Qy        732 AACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTTGTGAAAGAAAC 791
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Db        601 AACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTTGTGAAA-AAAC 659

Qy        792 CCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAA 851
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Db        660 CCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAA 719

Qy        852 GAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTACGCT-GGATGTT 910
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Db        720 GAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTATTTACGCTGGGATGTT 779

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Db        780 TGAGTGTGAAGAAATACGGGCCCAAGTACTGCGGTTTCCTGCGTGGGACGGCCCGATGCT 839

Qy        968 GCACGCCCCAGCTGACCAGGACTGTGAAGA 997
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RESULT 4
BQ222696

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LOCUS       BQ222696                866 bp    mRNA    linear   EST 02-MAY-2002
DEFINITION  AGENCOURT_7546349 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6025148
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ACCESSION   BQ222696
VERSION     BQ222696.1  GI:20404096
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 866)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13236  row: m  column: 21
            High quality sequence stop: 678.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
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                     Technologies."
BASE COUNT      222 a    230 c    240 g    174 t
ORIGIN
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  Matches  846;  Conservative    0;  Mismatches    4;  Indels    6;  Gaps    4;

Qy        185 AGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTCGGCG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 AGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTCGGCG 61

Qy        245 CCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGTGAAT 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGTGAAT 121

Qy        305 ATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAGTGCA 364
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Db        122 ATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAGTGCA 181

Qy        365 CATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTCCCCA 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        425 ACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTGGG 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        485 TCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGCAAGG 544
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Db        302 TCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGCAAGG 361

Qy        545 AGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCAGTTG 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 AGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCAGTTG 421

Qy        605 GAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTATACA 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTATACA 481

Qy        665 ACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCAAAGA 724
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 ACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCAAAGA 541

Qy        725 CCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTTGTGA 784
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 CCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTTGTGA 601

Qy        785 AAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTGAAAA 844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 AAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTGAAA- 660

Qy        845 AGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTACGCTG 904
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 --GGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTACGCTG 718
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Qy        905 GATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGC-GGTTCCTGCGTGGACGGCCGA 963
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        719 GATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGGTTCCTGCGTGGACGGCCGA 778

Qy        964 TGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATG-CGGTTCCGCTGCGAAGAT-GGGG 1021
              |||||||||||||| ||||||||||||||||||||| |||||||||||| ||||| ||||
Db        779 TGCTGCACGCCCCACCTGACCAGGACTGTGAAGATGCCGGTTCCGCTGCCAAGATGGGGG 838

Qy       1022 AGACATTTTCCAAGAA 1037
              ||||||||||| || |
Db        839 AGACATTTTCCCAGGA 854


RESULT 5
BQ644239
LOCUS       BQ644239                 939 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8207494 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6283134
            5', mRNA sequence.
ACCESSION   BQ644239
VERSION     BQ644239.1  GI:21768411
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 939)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CGAP (Stanford)
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2478  row: k  column: 07
            High quality sequence stop: 637.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6283134"
                     /clone_lib="NIH_MGC_100"
                     /tissue_type="hepatocellular carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
BASE COUNT      248 a    249 c     247 g    195 t
ORIGIN

  Query Match             67.2%;  Score 769.6;  DB 14;  Length 939;
  Best Local Similarity   94.6%;  Pred. No. 1.3e-202;
  Matches  808;  Conservative    0;  Mismatches   44;  Indels    2;  Gaps    1;

Qy        216 CACCAAGGGGCTGGAATGCAACTTCGGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAG 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CACCAAGGGGCTGGAATGCAACTTCGGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAG 60

Qy        276 AGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAAAG 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAAAG 120

Qy        336 TTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTGATGGCGCCGTGGGCTGCATTCC 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTGATGGCGCCGTGGGCTGCATTCC 180

Qy        396 TCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAA 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAA 240

Qy        456 AGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCCAT 515
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Db        241 AGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCCAT 300

Qy        516 GGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTT 575
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Db        301 GGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTT 360

Qy        576 GACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT 420

Qy        636 TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCA 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCA 480

Qy        696 AACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTAC 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTAC 540

Qy        756 CAATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTG 815
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTG 600

Qy        816 TGGACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATC 875
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGGACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATC 660

Qy        876 CCCCGAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAA 935
              ||||| |||||||| |||||||||||||||||||||||||||||   |||    | | || |
Db        661 CCCCGGACCAGTCAAGTTTACTTACGCTGGATGTTTGAGTGTGA--AAATACCGGCCCA 718

Qy        936 GTACTGCGGTTCCTGCGTGGACGGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAA 995
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GTACTGCGGTTCCTGCGTGGACGGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAA 778

Qy        996 GATGCGGTTCCGCTGCGAAGATGGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTC 1055
              |||||||||  |||| ||    |||     |  ||      |     | | ||||   |  |
Db        779 GATGCGGTTCGCCTGCCAAAGATGGGGAGAACATTTCCACAGAACGTCATGAATGATCC 838

Qy       1056 CTGCAAATGCAACT 1069
                 ||    |||| |
Db        839 AAGCCCTGGCAAAT 852


RESULT 6
AL550072
LOCUS       AL550072                 985 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL550072 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI040YC10 5
            prime, mRNA sequence.
ACCESSION   AL550072
VERSION     AL550072.1  GI:12886679
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 985)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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FEATURES             Location/Qualifiers
     source          1. .985
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DI040YC10"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      197 a    333 c    266 g    179 t     10 others
ORIGIN

  Query Match           66.5%;  Score 762.4;  DB 9;  Length 985;
  Best Local Similarity   98.8%;  Pred. No. 1.4e-200;
  Matches  771;  Conservative    6;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG 266

Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
              |||||||||||||||||:|||||||||||:|||||||||||||:||||||||||||||
Db        267 CTGGCGCTCTCCACCTGCSCCGCTGCCTGCSACTGCCCCCTGGAGGSGCCCAAGTGCGCG 326

Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 386

Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 446

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
              ||||||| :||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 GGCGCCA-STCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 505

Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 GAATATAAATCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 565

Qy        361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC 625

Qy        421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        626 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG 685

Qy        481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 745

Qy        541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        746 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTKATTGCA 805

Qy        601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTGGAATGGAGCCTCGCATCCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        806 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTGGAATGGAGCCTCGCATCCTA 865

Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        866 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCACACAACTTCATGGTCCCAGTGCTCA 925

Qy        721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
              ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        926 AAGACCTGTGGAAMTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 985


RESULT 7
BQ716204
LOCUS       BQ716204                876 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8101014 Lupski_sympathetic_trunk Homo sapiens cDNA clone
            IMAGE:6189946 5', mRNA sequence.
ACCESSION   BQ716204
VERSION     BQ716204.1  GI:21855101
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 876)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13587  row: p  column: 11
            High quality sequence stop: 663.
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                     /clone="IMAGE:6189946"
                     /clone_lib="Lupski_sympathetic_trunk"
                     /sex="male"
                     /tissue_type="sympathetic trunk"
                     /dev_stage="adult, 16 yr"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.9 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine); available through Life
                     Technologies."
BASE COUNT      228 a    228 c    229 g    190 t      1 others
ORIGIN

  Query Match           66.0%;  Score 756.2;  DB 14;  Length 876;
  Best Local Similarity   98.5%;  Pred. No. 6.8e-199;
  Matches  805;  Conservative    0;  Mismatches    8;  Indels    4;  Gaps    4;

Qy        269 TCTGCAGAGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTCCAGAATCTACCAAAACG 328
              |||    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCTTTGCAGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTCCAGAATCTACCAAAACG 60

Qy        329 GGGAAAGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTGATGGCGCCGTGGGCT 388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGGAAAGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTGATGGCGCCGTGGGCT 120

Qy        389 GCATTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGC 448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCATTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGC 180

Qy        449 TGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGG 508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGG 240
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Qy        509 ACCCCATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTCGATGCCTCCGAGG 568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCCCATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTCGATGCCTCCGAGG 300

Qy        569 TGGAGTTGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGC 628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGAGTTGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGC 360

Qy        629 TCCCTGTTTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTA 688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCCCTGTTTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTA 420

Qy        689 TTGTTCAAACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTCCACAC 748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTGTTCAAACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTCCACAC 480

Qy        749 GAGTTACCAATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGC 808
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GAGTTACCAATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGC 540

Qy        809 GGCCTTGTGGACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCA 868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCCTTGTGGACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCA 600

Qy        869 AGAAATCCCCCGAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACC 928
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGAAATCCCCCGAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACC 660

Qy        929 GGCCCAAGTACTGCGGTTCCTGCGTGGACGGCCGATGCTGCACGCCCCCAGCTGACCAGGA 988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGCCCAAGTACTGCGGTTCCTGCGTGGACGGCCGATGCTGCACGCCCCCAGCTGACCAGGA 720

Qy        989 CTGTG-AAGATGCGGTTCCGCTGCGAAGAT-GGGGAGACATTTTCCAAGAACGTCAT-GA 1045
              ||||| ||||||||| |||||||| ||||| ||||||||||||||||||||||||| ||
Db        721 CTGTGAAAGATGCGGGTCCGCTGCCAAGATGGGGGAGACATTTTCCAAGAACGTCATGGA 780

Qy       1046 TGATCCAGTCCTG-CAAATGCAACTACAACTGCCCGC 1081
              ||||||||||||| |||||||||||| ||||||| |
Db        781 TGATCCAGTCCTGCCAAATGCAACTACCACTGCCCCC 817


RESULT 8
BQ644666
LOCUS       BQ644666                992 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8510298 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6293429
            5', mRNA sequence.
ACCESSION   BQ644666
VERSION     BQ644666.1  GI:21768838
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 992)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CGAP (Stanford)
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2496  row: h  column: 06
            High quality sequence start: 17
            High quality sequence stop: 567.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:6293429"
                     /clone_lib="NIH_MGC_100"
                     /tissue_type="hepatocellular carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
BASE COUNT      268 a    257 c    258 g    208 t      1 others
ORIGIN

  Query Match             65.6%;  Score 751.6;  DB 14;  Length 992;
  Best Local Similarity   98.1%;  Pred. No. 1.4e-197;
  Matches  760;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy        214 CACACCAAGGGGCTGGAATGCAACTTCGGCGCCAGCTCCACCGCTCTGAAGGGGATCTGC 273
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 CCCACCAAGGGGCTGGAATGCAACTTCGGCGCCAGCTCCACCGCTCTGAAGGGGATCTGC 84

Qy        274 AGAGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAA 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 AGAGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAA 144

Qy        334 AGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTGATGGCGCCGTGGGCTGCATT 393
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTGATGGCGCCGTGGGCTGCATT 204

Qy        394 CCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGTC 453
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 CCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGTC 264

Qy        454 AAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCC 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 AAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCC 324

Qy        514 ATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTCGATGCCTCCGAGGTGGAG 573
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 ATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTCGATGCCTCCGAGGTGGAG 384

Qy        574 TTGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCT 633
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 TTGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCT 444

Qy        634 GTTTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTT 693
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 GTTTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTT 504

Qy        694 CAAACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTCCACACGAGTT 753
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 CAAACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTCCACACGAGTT 564

Qy        754 ACCAATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCT 813
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 ACCAATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGNCT 624

Qy        814 TGTGGACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAA 873
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 TGTGGACAGCCAGTGTACAGCAGCCCTGAAAAGGGCAAGAAATGCAGCAAGACCAAGAAA 684

Qy        874 TCCCCCGAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCC 933
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 TCCCCCGAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAAAAATACCGGCCC 744

Qy        934 AAGTACTGCGGTTCCTGCCGGAACGGCCGATGCTGCACGCCCCCAGCTGACCAGGA 988
              | |||||||||||||||| | |||||||||||||||| ||||| |||| | ||
Db        745 AGGTACTGCGGTTCCTGCCGGAACGGCCGATGCTGCACCCCCCACCTGAACCAGA 799
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RESULT 9
BG698245
LOCUS       BG698245                888 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602660158F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4803038 5',
            mRNA sequence.
ACCESSION   BG698245
VERSION     BG698245.1  GI:13965340
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 888)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10698  row: d  column: 15
            High quality sequence stop: 835.
FEATURES             Location/Qualifiers
     source          1. .888
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4803038"
                     /clone_lib="NCI_CGAP_Skn3"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      233 a    232 c    236 g    187 t
ORIGIN

  Query Match           65.4%;  Score 749.8;  DB 12;  Length 888;
  Best Local Similarity   98.0%;  Pred. No. 4.1e-197;
  Matches  801;  Conservative    0;  Mismatches   12;  Indels    4;  Gaps    4;

Qy        324 AAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTGATGGCGCCGT 383
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Db          1 AAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTGATGGCGCCGT 60

Qy        384 GGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCC 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCC 120

Qy        444 TCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTAT 503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTAT 180

Qy        504 CAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTCGATGCCTC 563
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTCGATGCCTC 240

Qy        564 CGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAA 623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAA 300

Qy        624 GCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAA 683
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Db        301 GCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAA 360

Qy        684 ATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTC 743
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTC 420

Qy        744 CACACGAGTTACCAATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGA 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACACGAGTTACCAATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGA 480

Qy        804 GGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAA 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAA 540

Qy        864 GACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAA 923
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAA 600

Qy        924 ATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGCCGATGCTGCACGCCCCAGCTGAC 983
              ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        601 ATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGG-CGATGCTGCACGCCCCAGCTGAC 659

Qy        984 CAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGGGAGACATTTTCCAAGAACGTCAT 1043
              ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db        660 CAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGGGAGTCATTTTCCAAGAACGTCAT 719

Qy       1044 GATGATCCAGTCCTGCAAATGCAACTACAACTGCCCGCATGCCAATGAAGCAGCGTTTCC 1103
              |||||||||| |||||||||||||||||| || |||||||||   |||||||||| ||
Db        720 GATGATCCAGT-CTGCAAATGCAACTACAAATG-CCGCATGCCATGAAAGCAGCGTTCCC 777

Qy       1104 CTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG 1140
              |||||||||||| || ||||| ||||| ||||  ||
Db        778 TTTCTACAGGCTGCTC-ATGACCTTCACCAATTAGGG 813


RESULT 10
AL513570
LOCUS       AL513570                1009 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  AL513570 LTI_NFL006_PL2 Homo sapiens cDNA clone XCL0BA001ZC03 5
            prime, mRNA sequence.
ACCESSION   AL513570
VERSION     AL513570.1  GI:12777064
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1009)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .1009
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="XCL0BA001ZC03"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      216 a    330 c    257 g    183 t     23 others
ORIGIN

  Query Match           65.3%;  Score 748.8;  DB 9;  Length 1009;
  Best Local Similarity   95.8%;  Pred. No. 8.4e-197;
  Matches  766;  Conservative   20;  Mismatches   12;  Indels    2;  Gaps    2;
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Qy          4 AGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGGCTG 63
              ||||||||||||||||||||||||||||||||:|||||||||||||||||||||:|||||||
Db        212 AGCTCCCGCATCGCCAGGGCGCTCGCCTTARTCGTCACCCTTCTCCACTTGAMCAGGCTG 271

Qy         64 GCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCGCCG 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db        272 GCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAARTGCGCGCCG 331

Qy        124 GGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTCAAC 183
              ||||| |||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db        332 GGAGTAGGGCTGGTCCGGGAMGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTCAAC 391

Qy        184 GAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTCGGC 243
              ||:||:|||||||||| ||||||||||||||:|||||||||||||||||||||||||:|||
Db        392 GARGAMTGCAGCAAAAAGCAGCCCTGCGACCAMACCAAGGGGCTGGAATGCAACTWCGGC 451

Qy        244 GCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGTGAA 303
              |||| | ||||||||||:|:|:|||||:||||:||||||||:|:|||||||:| ||||| ||
Db        452 GCCA-CACCACCGCTCTRAARGGGATMTGCARAGCTCAGTMARAGGGCARAACCTGTAAA 510

Qy        304 TATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAGTGC 363
              |||||:|||| |||||||||||||||||| ||||||||||||||||||||||||||||| |
Db        511 TATAAMTCCAAAATCTACCAAAACGGGGAAAATTTCCAGCCCAACTGTAAACATCAGTAC 570

Qy        364 ACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTCCCC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 ACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTCCCC 630

Qy        424 AACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTGG 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 AACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTGG 690

Qy        484 GTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGCAAG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 GTCTGTTACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGCAAG 750

Qy        544 GAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCAGTT 603
              |||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db        751 GAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAAAAATGAATTGATTKCAGTT 810

Qy        604 GGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTATAC 663
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Db        811 GGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTATAC 870

Qy        664 AACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCAAAG 723
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Db        871 AACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTKCTCAAAG 930

Qy        724 ACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTTGTG 783
              |||||||| |:|||||||||||||||||||||||||:|||||||| |||||||||||||
Db        931 ACCTGTGG-AMTGGTATCTCCACACGAGTTACCAATGAMAACCCTGAGTTCCGCCTTGTG 989

Qy        784 AAAGAAACCCGGATTTGTGA 803
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Db        990 AAAAAAACCCGGATTTGTGA 1009
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RESULT 11
BQ716992
LOCUS       BQ716992                 836 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8241315 Lupski_sympathetic_trunk Homo sapiens cDNA clone
            IMAGE:6187193 5', mRNA sequence.
ACCESSION   BQ716992
VERSION     BQ716992.1  GI:21855889
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 836)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13580  row: m  column: 18
            High quality sequence stop: 731.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6187193"
                     /clone_lib="Lupski_sympathetic_trunk"
                     /sex="male"
                     /tissue_type="sympathetic trunk"
                     /dev_stage="adult, 16 yr"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.9 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine); available through Life
                     Technologies."
BASE COUNT      215 a    221 c    235 g    165 t
ORIGIN

  Query Match           65.1%;  Score 746;  DB 14;  Length 836;
  Best Local Similarity   99.9%;  Pred. No. 4.5e-196;
  Matches  757;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy        139 CGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTCAACGAGGACTGCAGCAAA 198
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Db          1 CGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTCAACGAGGACTGCAGCAAA 60

Qy        199 ACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTCGGCGCCAGCTCCACCGCT 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTCGGCGCCAGCTCCACCGCT 120

Qy        259 CTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTCCAGAATC 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTCCAGAATC 180

Qy        319 TACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTGATGGC 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTGATGGC 240

Qy        379 GCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCC 438
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Db        241 GCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCC 300

Qy        439 AACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGAT 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGAT 360

Qy        499 AGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTCGAT 558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTCGAT 420

Qy        559 GCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCA 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCA 480

Qy        619 CTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGC 678
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Db        481 CTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGC 540

Qy        679 CAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGT 738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGT 600

Qy        739 ATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATT 798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATT 660

Qy        799 TGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAAGAAATGC 858
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Db        661 TGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAAGAAATGC 720

Qy        859 AGCAAGACCAAGAAAT-CCCCCGAACCAGTCAGGTTTA 895
              |||||||||||||||| ||||||||||||||||||||
Db        721 AGCAAGACCAAGAAATCCCCCCGAACCAGTCAGGTTTA 758
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RESULT 12
BQ720988
LOCUS BQ720988 908 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8103841 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:6190963 5', mRNA sequence.
ACCESSION BQ720988
VERSION BQ720988.1 GI:21859885
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 908)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13590 row: j column: 20
High quality sequence stop: 582.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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/clone_lib="Lupski_sympathetic_trunk"
/sex="male"
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/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."
BASE COUNT 237 a 224 c 246 g 200 t 1 others
ORIGIN

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  Query Match             64.5%;  Score 738.6;  DB 14;  Length 908;
  Best Local Similarity   98.7%;  Pred. No. 5.4e-194;
  Matches  755;  Conservative    0;  Mismatches    9;  Indels    1;  Gaps    1;

Qy        383 TGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACC 442
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Db          2 TGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACC 61

Qy        443 CTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTA 502
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Db         62 CTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTA 121

Qy        503 TCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTCGATGCCT 562
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Db        122 TCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTCGATGCCT 181

Qy        563 CCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGA 622
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Db        182 CCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGA 241

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Qy        683 AATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCT 742
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Qy        743 CCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTG 802
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Qy        803 AGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCA 862
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Db        422 AGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCA 481

Qy        863 AGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGA 922
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Qy        983 CCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG-GAGACATTTTCCAAGAACGTC 1041
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Db        602 CCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGGNGAGACATTTTCCCAGAACGTC 661

Qy       1042 ATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCGCATGCCAATGAAGCAGCGTTT 1101
              |||||||||||||||| |||||||||||||||||||||| | ||||||||||||||||
Db        662 ATGATGATCCAGTCCTGGCAATGCAACTACAACTGCCCGCATGGCCATGAAGCAGCGTTT 721

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Db        722 CCTTTCTACAGGTTGTTCAATGACATTCCCCAATTTAGGGACTAA 766
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RESULT 13
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LOCUS BQ719732 896 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8305072 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:6193402 5', mRNA sequence.
ACCESSION BQ719732
VERSION BQ719732.1 GI:21858629
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 896)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.

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            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM13596  row: p  column: 11
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                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.9 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine); available through Life
                     Technologies."
BASE COUNT      203 a    275 c    249 g    169 t
ORIGIN

  Query Match           63.4%;  Score 726;  DB 14;  Length 896;
  Best Local Similarity   96.4%;  Pred. No. 1.7e-190;
  Matches  796;  Conservative    0;  Mismatches   25;  Indels    5;  Gaps    5;

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Qy         61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG 120
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Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
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Qy        301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG 360
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Qy        541 AAGGAGCTGGGATTCGATGCCT-CCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGC 599
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Qy        659 TATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCT 718
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Db        705 TATACAACCCTTTACAGGCCAAAAAATGAATTGTTCAAACAACTTCATGGTCCCAGTGCT 764

Qy        719 CAAAGACCTGTGG-AACTGGTATCTCCACACGAG-TTACCAATGACAACCCTGAGTGCCG 776
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Db        765 CAAAGAACTGGGGAAACGGGTATCTCCCCCCGAGTTTACCATTGAAAACCCTGAGTGGCC 824

Qy        777 CCTTGTGAAAGAAA-CCCGGATTTGTGAGGTGCGGCCTTGTGGACA 821
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Db        825 CCCTGTGAAAAAAACCCCGGATTTGGGAAGTGCCGGCCTTGGGGCA 870


RESULT 14
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LOCUS       AL541592                929 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL541592 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE003YE20 5 prime
            , mRNA sequence.
ACCESSION   AL541592
VERSION     AL541592.1  GI:12872809
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 929)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B"
                     /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
                     cDNA was primed with a NotI-oligo(dT) primer. Five prime
                     end enriched, double-stranded cDNA was digested with NOt I
                     and cloned into the Not I and Eco RV sites of the
                     pCMVSPORT 6 vector.  Library was constructed by Life
                     Technologies. Contact : Feng Liang Life Technologies, a
                     division of Invitrogen 9800 Medical Center Drive Rockville
                     , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
                     fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      182 a    323 c    257 g    166 t      1 others
ORIGIN

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  Best Local Similarity   99.9%;  Pred. No. 1.5e-189;
  Matches  722;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 180
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Db        327 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC 386
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Qy        181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 240
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Db        387 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC 446

Qy        241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT 300
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Qy        661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
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Qy        721 AAG 723
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ACCESSION   BM479014
VERSION     BM479014.1  GI:18528056
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1083)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12289  row: c  column: 21
            High quality sequence stop: 596.
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                     oligo-dT primed. Average insert size 1.767 kb. Library
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                     Technologies. Note: this is a NIH_MGC Library."
BASE COUNT      275 a    314 c    242 g    252 t
ORIGIN
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  Query Match           62.3%;  Score 714;  DB 13;  Length 1083;
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Qy        303 ATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAGTG 362
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Qy        363 CACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTCCC 422
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Qy        423 CAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTG 482
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Qy        483 GGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGCAA 542
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Qy        902 CTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCC--TGCGTGGACGG 959
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Qy        960 CCGATGCTGCACGCCCCAGCTGACCAGGACTGTG-AAGATGCGGTTCCGCTGCGAAGATG 1018
              |||||||| |||||||| |||| ||||||| ||||| ||   || |
Db        721 CCGATGCTGAACGCCCCAGTTGACCAGGAAGGTGAAAGATGCCGTTCCCCTTGCAAAAAA 780

Qy       1019 GGGAGACATTTT 1030
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Db        781 TGGGGAAACATT 792
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Job time : 1915 secs